

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:18 ; Search time 40 Seconds

(Without alignment) 401.705 Million cell updates/sec

Title: US-10-617-955-2-COPY
Perfect score: 860
Sequence: 1 YSTEVEAVNLVNLYLRS.....VKSAGLGEVLFERLTALKHD 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.4

1: pir1,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID

Result	Score	Match	Length	DB	ID	Description
1	83.9	97.6	175	1	FRHOL	ferritin light cha
2	75.6	87.9	175	1	FRHOL	ferritin light chain - horse
3	74.5	86.6	175	2	JCT238	ferritin protein 1
4	73.8	85.8	175	2	S01239	ferritin light cha
5	72.6	84.4	183	1	FRFL	ferritin light cha
6	72.4	84.2	183	2	I54774	ferritin light cha
7	71.2	82.7	183	2	B33355	ferritin light cha
8	70.9	82.3	176	1	FRFL	ferritin, tadpole
9	53.5	62.2	176	2	A27805	ferritin chain H -
10	51.8	60.2	176	1	FRFL	ferritin heavy cha
11	51.3	59.7	176	2	C27805	ferritin chain M -
12	49.5	57.6	180	2	A26886	ferritin heavy cha
13	49.3	57.3	181	2	A29884	ferritin heavy cha
14	49.0	57.0	182	2	SL6070	ferritin heavy cha
15	48.7	56.6	183	1	FRHUF	ferritin heavy cha
16	48.1	55.9	164	1	A16710	ferritin, Soma - g
17	46.3.5	53.9	174	2	S45603	ferritin chain L -
18	45.7.5	53.2	174	2	B27805	hypothetical prote
19	42.2.5	49.1	170	2	T33854	hypothetical prote
20	38.9	45.3	170	2	T31870	ferritin heavy cha
21	38.7.5	45.1	172	1	A55628	ferritin - signal
22	38.2	44.4	181	2	S26251	ferritin heavy cha
23	37.5.5	43.7	173	1	B45628	ferritin, heavy cha
24	36.8	42.8	141	2	A18109	ferritin precursor
25	33.4.5	39.1	78	2	S06906	ferritin precursor
26	33.4.5	38.9	250	2	A40992	ferritin precursor
27	33.4.5	38.9	254	2	T08593	hypothetical prote
28	334.5	38.9	259	2	T47726	ferritin heavy cha
29	332	38.6	254	1	FRFBH	

ALIGNMENTS

RESULT 1
FRHOL
ferritin light chain - horse
C;Species: Equus caballus (domestic horse)
C;Accession: Q12Sep-1981 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
R;Takeda, S.; Ohta, M.; Ebina, S.; Nagayama, K.
Biochim. Biophys. Acta 1174, 218-220, 1993

A;Title: Cloning, expression and characterization of horse L-ferritin in Escherichia coli
A;Reference number: S36118
A;Accession: S36118
A;Molecule type: mRNA
A;Residues: 1-175 <TAK>
A;Cross-references: UNIPROT:P02791; GB:D14523; NID:9406208; PIDN:BA03396.1; PID:9406209
A;Experimental source: liver
A;Keywords: X-ray crystallography, ferritin, Heusterschreiter, W., Crichton, R.R., Bourne, P.E., Harrison, P.M.
X;REFSEQ: G.A.; Stansfield, R.D.; Bourne, P.E.; Harrison, P.M.
Nature 280, 298-300, 1980

A;Title: Helix packing and subunit conformation in horse spleen apo ferritin.
A;Reference number: A93239; MUID:0105459; PMID:7432529
A;Content: annotation; X-ray crystallography, 2.8 angstroms
C;Comment: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic
state, central cavity in which the polymeric ferric iron core is deposited.
C;Comment: There are two types of ferritin subunits: L (light) chain and H (heavy) chain.
C;Comment: In horse spleen the light chain is the major chain.

C;Superfamily: ferritin
C;Keywords: acetylated amino end, iron, iron storage, liver, metalloprotein, multimer, s

F;2-175/Product: ferritin light chain #status experimental <MAT>
F;2-Modifed site: acetylated amino end (Ser) (in mature form) #status experimental

F;54,57,58,61,64/Binding site: iron (Glu) #status predicted

Query Match 97.6%; Score 83.9; DB 1; Length 175;

Best Local Similarity 97.6%; Pred. No. 7.1e-64; Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YSTEVEAVNLVNLYLRSVTLISGFYFERDVALLEGCHFFRBLAEKREGARLLK 60
Db 9 YSTEVEAVNLVNLYLRSVTLISGFYFERDVALLEGCHFFRBLAEKREGARLLK 68

OY 61 MONQRGRALFDQDKPSQDWGTPDAMKAIVLEKSLNQALDHALGSKKADPHLC 120
Db 69 MONQRGRALFDQDKPSQDWGTPDAMKAIVLEKSLNQALDHALGSQAQDPHLCD 128

ferritin 3 precur
probable ferritin
ferritin 2 precur
ferritin 1 precur
ferritin 1 precur
ferritin 2 precur
ferritin precursor
ferritin H chain -
ferritin heavy cha
ferritin heavy cha
ferritin L chain -
ferritin precursor
ferritin light cha
ferritin - Thermot
ferritin like prot
artemin - brine sh

Db 129 FLESHFLDEEVKLIKKMGPfJINIORLVSSAGLGEYLFERLTIKHD 175

A;Cross-references: GB:119234; OMIM:134790
A;Map position: 19q13.3-19q13.4

A;Intron: 3/4/3

RESULT 2
FRUTL
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1983 #sequence_revision 03-May-1996 #text_change 09-Jul-2004

A;Note: the list of introns may not be complete

C;Complex: the functional molecule, composed of 24 chains, is roughly spherical with a c

(H) chain (see PIR:FETUH) and 1 light (L) chain.

C;Superfamily: ferritin

C;Keywords: acetylated amino end; iron; metalloprotein; multimer; storage protein

C;Modified site: acetylated amino end (Ser) (in mature form) #status predicted

R;Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.W.

J. Biol. Chem. 260, 11755-11761, 1985

A;Title: Structural and functional relationships of human ferritin H and L chains deduce

A;Reference number: A92494; MUID:86008223; PMID:3840162

A;Accession: B23920
A;Molecule type: mRNA

A;Residues: I-175 <BOY>

A;Cross-references: UNIPROT:P02792; GB:M1147; NID:9182513; PIDN:AA52439.1; PID:9182514

A;Title: Structure and expression of ferritin genes in a human promyelocytic cell line t

A;Reference number: A93087; MUID:87064341; PMID:3023856

A;Accession: B24844
A;Molecule type: mRNA

A;Residues: 33-175 <CHO>

A;Cross-references: GB:M12938; NID:912515; PIDN:AA52440.1; PID:9182516

R;Borner, M.H.; Saifeld, J.; Will, H.; Leibovitz, B.A.; Vass, J.K.; Munro, H.N.

Proc. Natl. Acad. Sci. U.S.A. 82, 3130-3143, 1985

A;Title: Structure of human ferritin light subunit messenger RNA: comparison with heavy

A;Reference number: A94043; MUID:85216457; PMID:3858810

A;Molecule type: mRNA

A;Residues: I-101, 'T', 103-175 <DOR>

A;Cross-references: GB:M10119; NID:9182517; PIDN:AA52831.1; PID:9182518

A;Experimental source: monocyte-like leukemia cell line U937

R;Addison, J.M.; Fitton, J.E.; Lewis, W.G.; May, K.; Harrison, P.M.

FEBS Lett. 164, 139-144, 1983

A;Title: The amino acid sequence of human liver apoferitin.

A;Reference number: A91317; MUID:84085077; PMID:6653779

A;Accession: A91317
A;Molecule type: protein

A;Residues: 2-36;41-53, 'Q', 55-86, 'Q', 88-174, 'ND' <ADD>

A;Experimental source: liver

A;Note: some peptides were positioned by homology

R;Muftifield, C.; Crichton, R.R.

FEBS Lett. 150, 43-48, 1982

A;Title: The amino acid sequence of human spleen apoferitin.

A;Reference number: A91308

A;Molecule type: protein

A;Residues: 2-18, 'Y', 20-25, 'Y', 27-39, 'BY', 42-152, 'RK', 155-175 <WUS>

A;Experimental source: spleen

A;Note: the order of residues 2-7, 40-41, and 153-154 was not determined. Some peptides

R;Santoro, C.; Marone, M.; Ferrone, M.; Costanzo, F.; Colombo, M.; Minganti, C.; Cortese

Nucleic Acids Res. 14, 2863-2876, 1986

A;Title: Cloning of the gene coding for human L apoferritin.

A;Reference number: 137137; MUID:86176772; PMID:3754330

A;Accession: 137137
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-83 <RES>

A;Cross-references: EMBL:X03742; NID:928518; PIDN:CAA27382.1; PID:28519

R;Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede,

Eur. J. Biochem. 239, 144-149, 1996

A;Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal ar

A;Reference number: S68911; MUID:96305378; PMID:8706699

A;Accession: S68943
A;Molecule type: protein

A;Residues: 84-89, 'E', 91-145-153, 'A', 155 <VLA>

A;Note: ferritin light chain 1

C;Comment: Ferritin stores iron after its oxidation to the ferric form. It is present in

A;Cross-references: GB:119234; OMIM:134790
A;Map position: 19q13.3-19q13.4

A;Intron: 3/4/3

A;Note: the list of introns may not be complete

C;Complex: the functional molecule, composed of 24 chains, is roughly spherical with a c

(H) chain (see PIR:FETUH) and 1 light (L) chain.

C;Superfamily: ferritin

C;Keywords: acetylated amino end; iron; metalloprotein; multimer; storage protein

C;Modified site: acetylated amino end (Ser) (in mature form) #status predicted

R;Daniels-McQueen, S.; Ray, A.; Walden, W.E.; Ray, B.K.; Brown, P.H.; Thach, R.E.

Query Match 87.9%; Score 756; DB 1; Length 175;
Best Local Similarity 86.2%; Pred. No. 7; Je-56%; Gaps 0; Indels 0; Mismatches 12;

Matches 143; Conservative 14; Mismatches 10; C;keywords: iron storage

QY 1 YSTEVEAVNLVNLVLYDASYTIVLSIGTYFDRDVALEGVCHFRELEKEKGAEILK 60

DB 9 YSTEVEAVNLVNLVLYDASYTIVLSIGTYFDRDVALEGVCHFRELEKEKGAEILK 68

QY 61 MONRGGRALFQDOKPDKEDWTGPMKAATVLEKSLNQALDLHALGSKKADPHCD 120

DB 69 MONRGGRALFQDOKPDKEDWTGPMKAATVLEKSLNQALDLHALGSKKADPHCD 128

QY 121 FLESHFLDEEVKLIKKMGPfJINIORLVSSAGLGEYLFERLTIKHD 167

DB 129 FLESHFLDEEVKLIKKMGPfJINIORLVSSAGLGEYLFERLTIKHD 175

RESULT 3

JC7238

ferritin protein light chain - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C;Accession: JC7238

R;Cheng, Q.; Gonzalez, P.; Ziegler Jr., J.S.

Biochem. Biophys. Res. Commun. 270, 349-355, 2000

A;Title: High level of ferritin light chain mRNA in lens.

A;Reference number: JC7238; MUID:20218664; PMID:10753629

A;Accession: JC7238
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-175 <CHE>

A;Cross-references: UNIPROT:O9JN8; GB:AF233445; PIDN:AAF36408.1

A;Experimental source: strain 13/N

C;Comment: This protein is an important regulator of oxidative stress and a primary factor

d is responsible for regulating the levels of intracellular iron.

C;Superfamily: ferritin

C;Keywords: iron storage

Query Match 86.6%; Score 745; DB 2; Length 175;

Best Local Similarity 85.6%; Pred. No. 6; Je-56%; Gaps 0; Indels 0; Mismatches 10;

Matches 143; Conservative 14; Mismatches 10; C;keywords: iron storage

QY 1 YSTEVEAVNLVNLVLYDASYTIVLSIGTYFDRDVALEGVCHFRELEKEKGAEILK 60

DB 9 YSTEVEAVNLVNLVLYDASYTIVLSIGTYFDRDVALEGVCHFRELEKEKGAEILK 68

QY 61 MONRGGRALFQDOKPDKEDWTGPMKAATVLEKSLNQALDLHALGSKKADPHCD 120

DB 69 MONRGGRALFQDOKPDKEDWTGPMKAATVLEKSLNQALDLHALGSKKADPHCD 128

QY 121 FLESHFLDEEVKLIKKMGPfJINIORLVSSAGLGEYLFERLTIKHD 167

DB 129 FLESHFLDEEVKLIKKMGPfJINIORLVSSAGLGEYLFERLTIKHD 175

RESULT 4

S0123

ferritin light chain - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: S01239

Nucleic Acids Res. 16, 7741, 1988

A;Title: Nucleotide sequence of cDNA encoding rabbit ferritin L chain.

A;Reference number: S01239; MUID:88319979; PMID:3412911

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P09451; EMBL:X07830; NID:91558; PIDN:CAA30682.1; PID:91559

C;Superfamily: ferritin

Query Match 85.8%; Score 738; DB 2; Length 175;

Best Local Similarity 85.6%; Pred. No. 2.5e-55; Mismatches 10; Indels 0; Gaps 0; Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 60

Db 9 YSPEVERAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 68

Qy 61 MONQRGGRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSKKADPHLC 120

Db 69 MNQRGGRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSAAHDPHLC 128

Qy 121 FLESHFLDEEVKLKLIKGMHDILNTIQLRVLKSKAGLGEYLPERLTKHD 167

Db 129 FLENHFLDEEVKLKGMHDILNTIRRLSGPOASLGEYLPERLTKHD 175

RESULT 5

FRTT_n
ferritin light chain - rat

C;Species: Rat/tub norvegicus (Norway rat)

C;Date: 28-Aug-1985 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

C;Accession: A29575; A0368

R;Lefbold, E.A.; Munro, H.N.

J. Biol. Chem. 262, 7335-7341, 1987

A;Title: Characterization and evolution of the expressed rat ferritin light subunit gene

A;Reference number: A29575; MUID:87222340; PMID:358416

A;Accession: A29575

A;Molecule type: DNA

A;Residues: 1183 <HEI>

A;Cross-references: UNIPROT:P02793; GB:J02741; NID:9204132; PIDN:AAA41155.1; PID:9204133

R;Lefbold, B.A.; Aziz, N.; Brown, A.J.P.; Munro, H.N.

J. Biol. Chem. 259, 4327-4334, 1984

A;Title: Conservation in rat liver of light and heavy subunit sequences of mammalian fer-

A;Reference number: A92474; MUID:84162134; PMID:6546756

A;Accession: A03268

A;Molecule type: mRNA

A;Residues: 257, 'K', 99-120, 'Q', 123-154, 'W', 156-183 <LE2>

A;Cross-references: GB:K01930; MUID:9204130; PIDN:AAA41154.1; PID:9204131

A;Note: initiator Met not shown

C;Comment: This ferritin mRNA was isolated from liver parenchymal cells.

C;Comment: The rat light chain has an octapeptide insertion after residue 158 compared w-

tains a central cavity in which the polymeric ferric iron core is deposited.

C;Comment: There are two types of ferritin subunits: L (light) chain and H (heavy) chain

C;Superfamily: ferritin

C;Keywords: iron storage; liver; multimer

Query Match 84.4%; Score 726; DB 1; Length 183;

Best Local Similarity 80.6%; Pred. No. 7.8e-54; Mismatches 9; Indels 8; Gaps 1; Matches 141; Conservative 17; Mismatches 9; Indels 8; Gaps 1;

Qy 1 YSTEVEAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 60

Db 9 YSPEVERAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 68

Qy 61 MONQRGGRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSKKADPHLC 120

Db 69 MNQRGGRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSAAHDPHLC 128

Qy 121 FLESHFLDEEVKLKLIKGMHDILNTIQLRVLKSKAGLGEYLPERLTKHD 167

Db 129 FLENHFLDEEVKLKGMHDILNTIRRLSGPOASLGEYLPERLTKHD 183

RESULT 6

ferritin light chain - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

R;Denis, M.G.

Int. J. Cancer 50, 930-936, 1992

A;Title: Isolation of cDNA clones corresponding to genes differentially expressed in two

A;Reference number: 154774; MUID:92210224; PMID:155892

A;Accession: 154774

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-183 <RES>

A;Cross-references: UNIPROT:P02793; GB:L01122; PIDN:AAA41152.1; PID:9204123

C;Superfamily: ferritin

Query Match 84.2%; Score 724; DB 2; Length 183;

Best Local Similarity 80.0%; Pred. No. 4e-54; Mismatches 10; Indels 8; Gaps 1; Matches 140; Conservative 17; Mismatches 10; Indels 8; Gaps 1;

Qy 1 YSTEVEAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 60

Db 9 YLNERGGRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSAAHDPHLC 128

Qy 121 FLESHFLDEEVKLKLIKGMHDILNTIQLRVLKSKAGLGEYLPERLTKHD 167

Db 129 FLENHFLDEEVKLKGMHDILNTIRRLSGPOASLGEYLPERLTKHD 183

RESULT 7

B33355
ferritin light chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Aug-1989 #sequence_revision 20-Dec-1989 #text_change 09-Jul-2004

C;Accession: B33355

R;Beaumont, C.; Dugast, I.; Renaudie, P.; Souroujon, M.; Grandchamp, B.

J. Biol. Chem. 264, 7498-7504, 1989

A;Title: Transcriptional regulation of ferritin H and L subunits in adult erythroid and

A;Accession: A33355

A;Reference number: B33355

A;Accession: B33355

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-113 <BEA>

A;Cross-references: UNIPROT:P29391; GB:J04716; NID:9193268; PIDN:AAA37614.1; PID:9309234

C;Superfamily: ferritin

Query Match 82.8%; Score 712; DB 2; Length 183;

Best Local Similarity 78.3%; Pred. No. 4.1e-53; Mismatches 13; Indels 8; Gaps 1; Matches 137; Conservative 17; Mismatches 13; Indels 8; Gaps 1;

Qy 1 YSTEVEAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 60

Db 9 YSPEVERAVNLVNLVYLASYTYSLGFFYFDDVALLEGVCHFRELAEKREGAERLIK 68

Qy 61 MONQRGGRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSKKADPHLC 120

Db 69 FONDROGRRALFQDQPSQDEWGTPDDAMKAIVAEKSLNQALDLHALGSAAHDPHLC 128

Qy 121 FLESHFLDEEVKLKLIKGMHDILNTIQLRVLKSKAGLGEYLPERLTKHD 167

Db 129 FLENHFLDEEVKLKGMHDILNTIRRLSGPOASLGEYLPERLTKHD 183

RESULT 8

FRFGL

territin; tadpole - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Accession: A37559; S12463; S05499; A40418
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C;Accession: A25627
 C;Accession: A25627
 R;Didsbury, J.R.; Theil, E.C.; Kaufman, R.E.; Dickey, L.F.
 J. Biol. Chem. 261, 949-955, 1986
 A;Title: Multiple red cell ferritin mRNAs' which code for an abundant protein in the embryo;
 A;Reference number: A25627; MUID:8608540; PMID:3484480
 A;Cross-references: UNIPROT:P07229; GB:MI12120; NID:9213691; PIDN:AAA49532.1; PID:9213692
 A;Experimental source: unicellular
 A;Accession: A25627; MUID:8608540; PMID:3484480
 A;Residues: 1-176 <DDID>
 A;Molecule type: mRNA
 A;Superfamily: ferritin
 C;Comment: The sequence of this ferritin is more similar to mammalian H chains than to I
 C;Keywords: erythrocyte; iron storage
 Query Match Best Local Similarity 62.3%; Score 536; DB 1; Length 176;
 Matches 96; Conservative 58.5%; Pred. No. 3e-38; 30; Indels 0; Gaps 0;
 C;Species: Rana catesbeiana (bullfrog)
 C;Accession: A27805
 C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
 C;Accession: A27805
 C;Accession: A27805
 Db 61 MONQGRGALFDQLQKSQDENGTTPDAMKAIIVLEKSLNQALDLHALGSKKADPHLCD 120
 QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 69 DONKRGGIVLQDVKEFPERDENNTLSMAQALQLEKTNVQALDLHKVGSKDKVDPHLCD 128
 QY . 121 FLESHFDEEVVKLIKKGDKHNLNIORLUVKSKAGLGEVLFERJTL 164
 Db 129 FLESEYLLEEQVKSIQKQGDYITNLKRIGLQPGONGMGEVLFDKHTM 172
 RESULT 9
 A27805
 ferritin chain H - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Accession: A27805
 C;Accession: A27805
 Db 61 MONQGRGALFDQLQKSQDENGTTPDAMKAIIVLEKSLNQALDLHALGSKKADPHLCD 120
 QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 69 DONKRGGIVLQDVKEFPERDENNTLSMAQALQLEKTNVQALDLHKVGSKDKVDPHLCD 128
 QY . 121 FLESHFDEEVVKLIKKGDKHNLNIORLUVKSKAGLGEVLFERJTL 164
 Db 129 FLESEYLLEEQVKSIQKQGDYITNLKRIGLQPGONGMGEVLFDKHTM 172
 RESULT 9
 A27805
 ferritin chain H - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Accession: A27805
 C;Accession: A27805
 Db 61 MONQGRGALFDQLQKSQDENGTTPDAMKAIIVLEKSLNQALDLHALGSKKADPHLCD 120
 QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 69 DONKRGGIVLQDVKEFPERDENNTLSMAQALQLEKTNVQALDLHKVGSKDKVDPHLCD 128
 QY . 121 FLESHFDEEVVKLIKKGDKHNLNIORLUVKSKAGLGEVLFERJTL 164
 Db 129 FLESEYLLEEQVKSIQKQGDYITNLKRIGLQPGONGMGEVLFDKHTM 172
 RESULT 9
 A27805
 ferritin chain H - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Accession: A27805
 C;Accession: A27805
 Db 61 MONQGRGALFDQLQKSQDENGTTPDAMKAIIVLEKSLNQALDLHALGSKKADPHLCD 120
 QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 69 DONKRGGIVLQDVKEFPERDENNTLSMAQALQLEKTNVQALDLHKVGSKDKVDPHLCD 128
 QY . 121 FLESHFDEEVVKLIKKGDKHNLNIORLUVKSKAGLGEVLFERJTL 164
 Db 129 FLESEYLLEEQVKSIQKQGDYITNLKRIGLQPGONGMGEVLFDKHTM 172
 RESULT 10
 A27805
 ferritin heavy chain - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Accession: C27805
 C;Date: 30-Sep-1991 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: C27805
 R;Didsbury, J.R.; Theil, E.C.; Kaufman, R.E.; Dickey, L.F.; Sreedharan, S.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.
 J. Biol. Chem. 262, 7901-7907, 1987
 A;Title: Differences in the regulation of messenger RNA for housekeeping and specialized ferritin heavy chain in amphibians
 A;Reference number: A92648; MUID:87222424; PMID:3495534
 A;Cross-references: UNIPROT:P07229; GB:MI15655; NID:9213672; PIDN:AAA49523.1; PID:9213673
 A;Accession: A27805
 A;Residues: 1-176 <DDID>
 A;Molecule type: mRNA
 A;Superfamily: ferritin
 A;Accession: A27805
 A;Accession: A27805
 Db 61 MONQGRGALFDQLQKSQDENGTTPDAMKAIIVLEKSLNQALDLHALGSKKADPHLCD 120
 QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 69 DONKRGGIVLQDVKEFPERDENNTLSMAQALQLEKTNVQALDLHKVGSKDKVDPHLCD 128
 QY . 121 FLESHFDEEVVKLIKKGDKHNLNIORLUVKSKAGLGEVLFERJTL 164
 Db 129 FLESEYLLEEQVKSIQKQGDYITNLKRIGLQPGONGMGEVLFDKHTM 172
 RESULT 11
 C27805
 ferritin chain M - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Accession: C27805
 C;Accession: C27805
 R;Didsbury, J.R.; Theil, E.C.; Kaufman, R.E.; Dickey, L.F.; Sreedharan, S.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.;
 J. Biol. Chem. 262, 7901-7907, 1987
 A;Title: Differences in the regulation of messenger RNA for housekeeping and specialized ferritin heavy chain in amphibians
 A;Reference number: A92648; MUID:87222424; PMID:3495534
 A;Accession: C27805

A;Molecule type: mRNA
A;Residues: 1-176 <DIC>
A;Cross-references: UNIPROT:P07798; GB:J02724; NID:9213676; PIDN:AAA49525.1; PID:9213677
C;Superfamily: ferritin

Query Match 59.7%; Score 513; DB 2; Length 176;
Best Local Similarity 57.6%; Pred. No. 2.6e-36; Mismatches 34; Indels 0; Gaps 0;
Matches 95; Conservative 36; Residues 95; Conservatve 36; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYRASVTYLSIGFYFRDDVALEGVCHFRELAERKREGALERLK 60
Db 9 YHSDCEBAVNMLNLYASITYSSMYAFFPDRDVAVHNVAEFFKSHBERAEAKFM 68
Qy 61 MONORGGRALFQDLOPKSQDEWGTPDAMGAIYVLEKSINQALDIHALGSKKADPHCD 120
Db 69 YONKGGRGVVLFQDIPKPERBWTGLEAMORALOEKTQNQALDQBLHKLATKDVKDPHLC 128
Qy 121 FLESHFLDEEVKLIKONGDHNTIQRLVSKAGLGEYLFRFLTG 165
Db 129 FLESEVLEEQVKDQDKRIGDFITNUKRLGPENGMBGFLFDKHSVK 173

RESULT 12

A26886

ferritin heavy chain - chicken

C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004

R;Stevens, P.W.; Dodgeon, J.B.; Engel, J.D.
Mol. Cell. Biol. 7, 1751-1758, 1987
A;Title: Structure and expression of the chicken ferritin H-subunit gene.
A;Reference number: A26886; MUID:87257874; PMID:3600643

A;Accession: A26886

A;Molecule type: DNA
A;Residues: 1-180 <STE>
A;Cross-references: UNIPROT:P08267; GB:M16343; NID:9211773; PIDN:AAA48766.1; PID:9211774
C;Genes:
A;Locations: 37/3; 86/3; 128/3
C;Superfamily: ferritin

Query Match 57.6%; Score 495; DB 2; Length 180;
Best Local Similarity 53.7%; Pred. No. 9e-35; Mismatches 38; Indels 0; Gaps 0;
Matches 88; Conservative 38; Residues 88; Conservatve 38; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYRASVTYLSIGFYFRDDVALEGVCHFRELAERKREGALERLK 60
Db 12 YHQDCERAINRQINLNLVYASVTYLSIGFYFRDDVALEGVCHFRELAERKREGALERLK 71

RESULT 13

A39884

ferritin heavy chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004

D;Accession: A39884; A05251; A15903; 152222

Qy 61 MONORGGRALFQDLOPKSQDEWGTPDAMGAIYVLEKSINQALDIHALGSKKADPHCD 120
Db 72 LONORGGRIFLQDIPKPERBWTGLEAMORALOEKTQNQALDQBLHKLATKDVKDPHLC 131

Qy 121 FLESHFLDEEVKLIKONGDHNTIQRLVSKAGLGEYLFRFLTG 165
Db 132 FIETHYLINEQVKSIKEGLHDVTLRKGMAGPESGMAYLFDKHTLG 175

RESULT 14

S06070

ferritin heavy chain - mouse

C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

D;Accession: S06070; JH0229; S01948; A31113; A33355

R;Yachou, A.K.; Renaudie, F.; Grandchamp, B.; Beaumont, C.

Nucleic Acids Res. 17, 8005, 1989

A;Title: Nucleotide sequence of the mouse ferritin H chain gene.
A;Reference number: S06070; MUID:9016900; PMID:2798146
A;Accession: S06070
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-182 <YAC>
A;Cross-references: UNIPROT:P09528; GB:X52561; EMBL:X15404; NID:950953; PIDN:CAA36795.1;
A;Residues: 1-182 <YNA>
A;Accession: A39884
A;Cross-references: UNIPROT:P19132; GB:M18053; NID:9204126; PIDN:AAA41153.1; PID:9204126
A;Molecule type: DNA
A;Residues 1-181 <MBP>
A;Cross-references: UNIPROT:P19132; GB:M18053; NID:9204126; PIDN:AAA41153.1; PID:9204126
R;Leibold, E.A.; Aziz, N.; Brown, A.J.P.; Munro, H.N.

J. Biol. Chem. 259, 4327-4334, 1984
A;Title: Conservation in rat liver of light and heavy subunit sequences of mammalian ferritin heavy chain
A;Reference number: A82474; MUID:84162134; PMID:6546756

A;Accession: A05251

A;Molecule type: protein
A;Residues: 158-180 'E' <LEI>
A;Experimental source: liver
R;Huberman, A.; Barahona, B.
Biochim. Biophys. Acta 533, 51-55, 1978
A;Title: Primary structure of rat liver apoferritin. The amino end.

A;Accession: A15903

A;Molecule type: protein
A;Residues: 4-67 <HUB>
A;Experimental source: liver
R;Ursini, M.V.; de Franciscis, V.
Biochem. Biophys. Res. Commun. 150, 287-295, 1988
A;Title: TSH regulation of ferritin H chain messenger RNA levels in the rat thyroids.
A;Reference number: I52222; MUID:88106597; PMID:2827671
A;Accession: I52222
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 136-181 <RES>
A;Cross-references: GB:M29330; NID:9207527; PIDN:AAA42300.1; PID:9207528
C;Superfamily: ferritin

C;Keywords: acetylated amino end; iron storage
F;4/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 57.3%; Score 493; DB 2; Length 181;
Best Local Similarity 53.0%; Pred. No. 1.3e-34; Mismatches 38; Indels 0; Gaps 0;
Matches 88; Conservative 38; Residues 88; Conservatve 38; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYRASVTYLSIGFYFRDDVALEGVCHFRELAERKREGALERLK 60
Db 12 YHQDCERAINRQINLNLVYASVTYLSIGFYFRDDVALEGVCHFRELAERKREGALERLK 71

RESULT 15

Qy 61 MONORGGRALFQDLOPKSQDEWGTPDAMGAIYVLEKSINQALDIHALGSKKADPHCD 120
Db 72 LONORGGRIFLQDIPKPERBWTGLEAMORALOEKTQNQALDQBLHKLATKDVKDPHLC 131

Qy 121 FLESHFLDEEVKLIKONGDHNTIQRLVSKAGLGEYLFRFLTG 165
Db 132 FIETHYLINEQVKSIKEGLHDVTLRKGMAGPESGMAYLFDKHTLG 177

RESULT 16

R;Jiang, Y.; Setoguchi, M.; Higuchi, Y.; Yoshida, S.; Arizuki, S.; Yamamoto, S.
R;Mirazaki, Y.; Setoguchi, M.; Higuchi, Y.; Yoshida, S.; Arizuki, S.; Yamamoto, S.
Nucleic Acids Res. 16, 10373, 1988

A;Title: Nucleotide sequence of cDNA encoding the heavy subunit of mouse macrophage ferritin
A;Reference number: S01948; MUID:89057487; PMID:3194211

A;Accession: S01948
A;Molecule type: mRNA
A;Residues: 1-182 <NMY>
A;Cross-references: EMBL:X12812; NID:950951; PIDN:CAA31300_1; PID:950952
R;Torti, S.V.; Kwak, E.L.; Miller, S.C.; Miller, L.L.; Ringold, G.M.; Myambu, K.B.; Youn J. Biol. Chem. 260, 11755-11761, 1985
A;Title: The molecular cloning and characterization of murine ferritin heavy chain, a tu
A;Reference number: A31113; MUID:88315064; PMID:3410854
A;Molecule type: mRNA
A;Residues: 1-182 <TOR>
A;Cross-references: GB:J03941; NID:9193264; PIDN:AAA17611_1; PID:9309232
R;Braumont, C.; Dugast, I.; Renaudie, F.; Souroujon, M.; Grandchamp, B.
J. Biol. Chem. 264, 7498-7504, 1989
A;Title: Transcriptional regulation of ferritin H and L subunits in adult erythroid and
ferritin shell.
A;Reference number: A33355; MUID:89214195; PMID:2708374
C;Genetics:
A;Introns: 38/3; 87/3; 129/3
C;Superfamily: ferritin

RESULT 15

FRHHL
ferritin heavy chain - human
N;Alternate names: apoferitin H; ferritin heavy polypeptide 1
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: A23517; A2045; JN0571; A23920; A2444; A03265; A05250; PN0562
R;Costanzo, P.; Colombo, M.; Staemmler, S.; Santoro, C.; Marone, M.; Frank, R.; Delius, Nucleic Acids Res. 14, 721-736, 1986
A;Title: Structure of gene and pseudogenes of human apoferitin H.
A;Reference number: A23517; MUID:86120367; PMID:3003694
A;Molecule type: DNA
A;Residues: 1-183 <COS>
A;Cross-references: UNIPROT:P02794; GB:X03487; NID:931340; PIDN:CAA27205_1; PID:9762940; R;Hentze, M.W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi, W.; Drysdale, J.; Leonard Proc. Natl. Acad. Sci. U.S.A. 83, 7226-7230, 1986
A;Title: Cloning, characterization, expression, and chromosomal localization of a human A;Reference number: A25045; MUID:87016920; PMID:3020541.
A;Accession: A25045
A;Molecule type: DNA
A;Residues: 1-183 <HEN>
A;Cross-references: GB:MI4211; GB:MI4212; NID:9182509; PIDN:AAA52438_1; PID:9182511; GB:
R;Dhar, M.; Chauthaiwale, V.; Joshi, J.G.
Gene 126, 275-278, 1993
A;Title: Sequence of a cDNA encoding the ferritin H-chain from an 11-week-old human feta A;Reference number: JN0571; MUID:3246257; PMID:916709
A;Accession: JN0571

Query Match 57.0%; Score 490; DB 2; Length 182;
Matches 88; Conservative 53.0%; Prede. No. 2.4e-34; Indels 0; Gaps 0;
Query 1 YSTEVEAVNLVNLVLYLASYTVLGKFYFDRDVALLALEGVCHFFRELAEKKGREGAEERLLK 60
Db 13 YHQDSEAAINRQINLVELYASVYVLSMSYFDRDVALKNFAKYFLHQSHHEEREHAEKLK 72
Query 61 MNQRGGRAFLQDQIKPQSPQDWGTPDAMKAALVLEKSLNQALDHIALGSKKADPHLC 120
Db 73 LQNQRGGRIFLQDQIKPPCDWGLNMECALHLEKVSUNQSLHLKLTAKDNDPHLC 132
Query 121 PLESHRLDEEVKLLIKQMDHINIQLRKVSKAGLGLYFLFRPLTKL 166
Db 133 PIETVYLSEQVKSIKELGHDVTLRKMGAPESAGMABYLFDFDKHTLH 178

A;Molecule type: mRNA
A;Residues: 1-183 <DHA>
A;Cross-references: GB:MN97164; NID:9306743; PIDN:AAA35832_1; PID:9306744
R;Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.W.
J. Biol. Chem. 260, 11755-11761, 1985
A;Title: Structural and functional relationships of human ferritin H and L chains deduced A;Reference number: A22494; MUID:86008223; PMID:3840162
A;Accession: A23920
A;Cross-references: GB:ML1146; NID:9182504; PIDN:AAA52437_1; PID:9182505
R;Chou, C.C.; Gatti, R.A.; Fuller, M.L.; Concamon, P.; Wong, A.; Chada, S.; Davis, R.C., Mol. Cell. Biol. 6, 565-573, 1986
A;Title: Structure and expression of ferritin genes in a human promyelocytic cell line t
A;Reference number: A303087; MUID:87064341; PMID:3023856
A;Accession: A24844
A;Molecule type: mRNA
A;Residues: 1-183 <CHO>
A;Cross-references: GB:ML2337; NID:9182506; PIDN:AAA35830_1; PID:9182507
A;Note: the authors translated the codon CAG for residue 113 as Glu
R;Costanzo, F.; Santoro, C.; Colantuoni, V.; Bensi, G.; Raugei, G.; Romano, V.; Cortese, EMBO J. 3, 23-27, 1984
A;Title: Cloning and sequencing of a full length cDNA coding for a human apoferitin H ct
A;Reference number: A33269; MUID:84158535; PMID:6323167
A;Accession: A03269
A;Molecule type: mRNA
A;Residues: 1-175; WETVIMKAKPRANFP' <CO2>
A;Cross-references: GB:X00318; NID:928434; PIDN:CAA25086_1; PID:928435
A;Note: this sequence has been revised in reference A23517
R;Luzzago, A.; Felici, F.; Tramontano, A.; Pesci, A.; Cortese, R.
Gene 128, 51-57, 1993
A;Title: Mimicking of discontinuous epitopes by phage-displayed peptides, I. Epitope map.
A;Reference number: PN0562; MUID:93285469; PMID:7683301
A;Contents: annotation; artificial epitopes
R;Lawson, D.M.; Artyukh, P.J.; Yewdall, S.J.; Smith, J.M.A.; Livingstone, J.C.; Treffry, Nature 349, 541-544, 1991
A;Title: Solving the structure of human H ferritin by genetically engineering intermolecul
A;Reference number: A57130; MUID:9125486; PMID:1992356
A;Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 6-86' Q', 88-177
C;Comment: There are several distinct binding sites for iron. Two sites each consist of t
ay bind several iron atoms and possess ferroxidase activity.
C;Genetics:
A;Gene: GDB:FTHL6
A;Cross-references: GDB:120617; OMIM:134770
A;Map position: 11q12-11q13
A;Introns: 38/3; 87/3; 129/3
C;Complex: The functional molecule, composed of 24 chains, is roughly spherical with a ce
(H) chain and light (L) chain (see PIR:FTHL6). The predominant chain can be light or he
C;Function:
A;Description: intracellular protein that stores and transports iron in a soluble, nonto,
A;Note: tissues containing high levels of iron and involved in long-term storage tend to
C;Superfamily: ferritin
C;Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
F;28, 62, 63, 65, 66, 108/Binding site: iron (Glu, Glu, Glu, His, Glu) #status experimental
F;85/Binding site: iron (Asp) (shared with tetrameric partners) #status experimental
F;87/Binding site: iron (Iys) (shared with tetrameric partners) #status experimental

Query Match 56.6%; Score 487; DB 1; Length 183;
Matches 87; Conservative 53.0%; Prede. No. 4.3e-34; Indels 0; Gaps 0;
Query 1 YSTEVEAVNLVNLVLYLASYTVLGKFYFDRDVALLALEGVCHFFRELAEKKGREGAEERLLK 60
Db 13 YHQDSEAAINRQINLVELYASVYVLSMSYFDRDVALKNFAKYFLHQSHHEEREHAEKLK 72
Query 61 MNQRGGRAFLQDQIKPQSPQDWGTPDAMKAALVLEKSLNQALDHIALGSKKADPHLC 120
Db 73 LQNQRGGRIFLQDQIKPPCDWGLNMECALHLEKVSUNQSLHLKLTAKDNDPHLC 132
Query 121 PLESHRLDEEVKLLIKQMDHINIQLRKVSKAGLGLYFLFRPLTKL 164
Db 133 PIETVYLSEQVKSIKELGHDVTLRKMGAPESAGMABYLFDFDKHTLH 178

Tue Aug 23 10:27:26 2005

us-10-617-955-2-copy.rpr

Page 7

Search completed: August 22, 2005, 09:10:52
Job time : 41 secs

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Om protein - protein search, using bw model

Run on: August 22, 2005, 09:06:17 ; Search time 42 Seconds

Sequence: 1 YSTEVEAVNRVNLVYRAS..... VRSKAGLGEYLFERLTQH D 167
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Title: US-10-617-955-2-COPY
 Perfect score: 860
 Sequence: 1 YSTEVEAVNRVNLVYRAS..... VRSKAGLGEYLFERLTQH D 167
 Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgnt2_6/prodata1/iaa/5A_COMB_pep:
 2: /cgnt2_6/prodata1/iaa/5B_COMB_pep:
 3: /cgnt2_6/prodata1/iaa/6A_COMB_pep:
 4: /cgnt2_6/prodata1/iaa/6B_COMB_pep:
 5: /cgnt2_6/prodata1/iaa/PCITS_COMB_pep:
 6: /cgnt2_6/prodata1/iaa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	87.9	175	4	US-09-919-09-333
2	731	85.0	228	4	US-09-949-06-10795
3	487	56.6	220	4	US-09-949-06-10773
4	334	38.8	250	4	US-09-418-830-2
5	334	38.8	250	4	US-09-418-830-3
6	256	29.8	243	2	US-09-829-110-3
7	221	25.7	107	4	US-09-621-976-4402
8	168	17.0	168	3	US-09-134-01C-4664
9	94	10.9	162	4	US-09-602-772A-362
10	88	10.2	175	4	US-09-689-09A-14335
11	83.5	9.7	644	3	US-09-300-09-18
12	82.5	9.6	168	4	US-09-543-681A-7822
13	82	9.5	998	4	US-09-198-432A-841
14	82	9.5	998	4	US-09-438-183A-793
15	80.5	9.4	629	3	US-09-300-09-19
16	80	9.3	277	4	US-09-602-77A-8
17	79	9.3	514	4	US-09-902-540-10406
18	79	9.2	719	4	US-09-763-90B-5
19	77.5	9.0	390	4	US-09-107-522A-6425
20	77.5	9.0	482	4	US-09-902-540-16249
21	77	9.0	502	4	US-09-949-06-7837
22	77	9.0	302	4	US-09-270-767-59138
23	77	9.0	501	4	US-09-210-67-43743
24	76.5	8.9	491	4	US-09-248-796A-19512
25	76	8.8	7831	4	US-09-902-540-12902
26	8.7	8.7	374	4	US-09-710-278-1562
27	8.7	8.7	397	3	US-09-134-001C-4104

ALIGNMENTS

RESULT 1
 US-09-919-039-333
 Sequence 333, Application US/09919039
 Patent No. 6727066
 GENERAL INFORMATION:
 APPLICANT: Kaser, Matthew R.
 TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 FILE REFERENCE: PA-0035 US
 CURRENT APPLICATION NUMBER: US/09/919, 039
 CURRENT FILING DATE: 2002-09-09
 PRIOR APPLICATION NUMBER: 60/222,113
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 401
 SOFTWARE: PERL Program
 SBO ID NO: 333
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. 6727066 4005778CDI
 ;

Query Match 87.9%; Score 756; DB 4; Length 175;
 Best Local Similarity 86.2%; Pred. No. 9.6-73;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 Sequence 333, App
 Sequence 10295, A
 Sequence 10773, A
 Sequence 2, Appli
 Sequence 3, Appli
 Sequence 3, Appli
 Sequence 4402, Ap
 Sequence 4664, Ap
 Sequence 362, App
 Sequence 14335, A
 Sequence 18, Appli
 Sequence 7822, Ap
 Sequence 841, App
 Sequence 793, App
 Sequence 19, Appli
 Sequence 8, Appli
 Sequence 10405, A
 Sequence 5, Appli
 Sequence 6425, Ap
 Sequence 16249, A
 Sequence 7837, Ap
 Sequence 59138, A
 Sequence 43743, A
 Sequence 19312, A
 Sequence 12902, A
 Sequence 1562, Ap
 Sequence 10935, A
 Sequence 19, Appli
 Sequence 83, Appli
 Sequence 82, Appli
 Sequence 54, Appli
 Sequence 12447, A
 Sequence 27933, A
 Sequence 10427, A
 Sequence 16251, A
 Sequence 13, Appli
 Sequence 17, Appli
 Sequence 19, Appli

QY 1 YSTEVEAVNRVNLVYRAS..... VRSKAGLGEYLFERLTQH D 167
 Db 9 YSTDVEAVNLVNLVQASYTYSLGFYFDRDDVALLEGVSHFFRELAKREGYERLK 68
 QY 61 MONORGGRALFQDLQPKSDQEWGTPDAMGAIVLEKSINQALDLHALGSKKADPHLC 120
 Db 69 MONORGGRALFQDLQPKSDQEWGTPDAMKALEKUNKQALDLHALGSARTDPHLCD 128
 QY 121 PFLSHFLDEEVKLIGKGDHLTNIGRLVSKAGLGEYLFERLTQH 167
 Db 129 PFLTHFLDEEVKLIGKGDHLTNIGRLVSKAGLGEYLFERLTQH 175

RESULT 2
 US-09-949-016-10295
 ; Sequence 1095, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; TITLE OF INVENTION: FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016

RESULT 3
US-09-949-016-1073
; Sequence 1073, Application US/09949016
; Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL0010107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1073
LENGTH: 220
TYPE: PRT
; ORGANISM: Human
; US-09-949-016-1073

Query Match 85.0%; Score 731; DB 4; Length 238;
Best Local Similarity 84.3%; Pred. No. 6.8e-70; Mismatches 10; Indels 0; Gaps 0;
Matches 140; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVLRASTYTLISGYFRRDVALLEGVCHFFRELAEEKREGAERLKK 60
Db 72 YSTDVERAVANVNLVNLVLQASTYTLISGYFRRDVALLEGVSHFFRELEEKREGYERLIK 131
QY 61 MNQRGGRALPQDLOKPSDQEWGTPDAMKAATIVLKSKLNAQOALDHIALGSSKKADPHLCID 120
132 MNQRGGRALPQDLOKPSDQEWGTPDAMKAALMALKKQNAQOALDHIALGSSKKADPHLCID 191
QY 121 FLESHLDDEKLKIKMGDHNTIQLVKSKAGLGEYLPERLTIKH 166
192 FLETHLDDEEVKLKIKMGDHNTLHLGGPERAGLGEYLPERLTIKH 237
Db ;

RESULT 4
US-09-418-830-2
; Sequence 2, Application US/09418830
; Patent No. 6563019
GENERAL INFORMATION:
APPLICANT: Deak, Maria
APPLICANT: Dudit, Denes
APPLICANT: Torok, Karolyne
APPLICANT: Sas, Laszlo
APPLICANT: Barna, Balazs
APPLICANT: Kiraly, Zoltan
TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
FILE REFERENCE: DEAK
CURRENT APPLICATION NUMBER: US/09/418,830
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: PCV/GB98/01108
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 2
LENGTH: 250
TYPE: PRT
; ORGANISM: Medicago sativa
; US-09-418-830-2

RESULT 5
US-09-418-830-3
; Sequence 3, Application US/09418830
; Patent No. 6563019
GENERAL INFORMATION:
APPLICANT: Deak, Maria
APPLICANT: Dudit, Denes
APPLICANT: Torok, Karolyne
APPLICANT: Sas, Laszlo
APPLICANT: Barna, Balazs
APPLICANT: Kiraly, Zoltan
TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
FILE REFERENCE: DEAK
CURRENT APPLICATION NUMBER: US/09/418,830
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR FILING DATE: 1997-09-22
PRIOR APPLICATION NUMBER: HU 9700762
PRIOR APPLICATION NUMBER: PCV/GB98/01108
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 6

Query Match 56.6%; Score 487; DB 4; Length 220;
Best Local Similarity 53.0%; Pred. No. 6.4e-44; Mismatches 37; Indels 0; Gaps 0;
Matches 87; Conservative 40; Mismatches 37; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVLRASTYTLISGYFRRDVALLEGVCHFFRELAEEKREGAERLKK 60
Db 50 YHQDSEMAINQNLVNLVLQASTYTLISGYFRRDVALLEGVSHFFRELEEKREGAERLKK 109
QY 61 MNQRGGRALPQDLOKPSDQEWGTPDAMKAATIVLKSKLNAQOALDHIALGSSKKADPHLCID 120
110 MNQRGGRALPQDLOKPSDQEWGTPDAMKAALMALKKQNAQOALDHIALGSSKKADPHLCID 169
QY 121 FLESHLDDEKLKIKMGDHNTIQLVKSKAGLGEYLPERLTIKH 164
170 FLETHLDDEEVKLKIKMGDHNTLHLGGPERAGLGEYLPERLTIKH 213
Db ;

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 3 ; LENGTH: 250

; LENGTH: 250

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE: OTHER INFORMATION: Description of Unknown organism: we do not have ; OTHER INFORMATION: this information

; US-09-418-830-3

Query Match Best Local Similarity 33%; Pred. No. 3.1e-19; Length 243; Matches 71; Conservative 3%; Mismatches 42%; Indels 34; Gaps 7;

Best Local Similarity 42.4%; Pred. No. 1.6e-27; Length 250; Matches 72; Conservative 38; Mismatches 52; Indels 8; Gaps 3;

Query 1 YSTEVEAVNRLVNLRYLASYTIVLSGFYFDRDVDALEGVCHFFRERAEKREGAERLLK 60

Db 9 VSTDEBAVNVLVNLQASITYLSGFYFDRDVDALEGVSHFFRERAEQAQL---- 63

Query 85 YQDVESETNEQINTEVNVSYVHSLFAYFDRDNALKGLAKFFKESSBEREHAELMR 144

Db 61 MQNQGGRALFQDLQPSQD---EWGTFPDAMKAIVLEKSLNQALDHALGSKKADP 116

Query 145 YQNTFFGRVVLHPTSPSPEDPHAKGDALYAMEALSLIKLVNLNTHSVAARNNDP 204

Db 117 HLCDFPLESHFLDEBEVKLKGDKHNTIQRLVSKAGLGHYLFERDLTKH 166

Query 205 QLANTESEFLEQEVESIKKISEYTLQRLVGK--GHGWHDFFD-TILH 250

Db 112 KADPHLCDESHLDEEKL----IKMDGHDTNLIPLVK 149

Query 64 -----RASPEDKAPWRSIDHSDGSSSSHLQSKTAKWAASLENLIEDPE--GV 114

Db 115 KR---FREEKKFSEENVLFWLACEDFKKNQDK-TOMQEK 153

RESULT 6 US-08-829-110-3

; Sequence 3 Application US/08029110

; Patent No. 5882830

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN

; TITLE OF INVENTION: SIGNALING

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

ZIPP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829, 110

FILING DATE: Filed Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billing, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0259 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-0555

TELEFAX: 415-845-4116

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 243 amino acids

TYPE: amino acid

STRANDBNESS: single

TOPOLOGY: linear

LITERATURE:

IMMEDIATE SOURCE:

CLONE: 343504

RESULT 7 US-08-621-976-4402

; Sequence 4402 Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; CURRENT APPLICATION NUMBER: US/09/621, 976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.Pm

; SEQ ID NO: 4402

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-621-976-4402

Query Match Best Local Similarity 40.2%; Pred. No. 5.4e-16; Length 107; Matches 43; Conservative 24; Mismatches 40; Indels 0; Gaps 0;

Query 26 LGFYFDRDVDALEGVCHFFRERAEKREGAERLLKMONORGSGRALFQDLQPSQDSWGT 85

Db 1 MAFYFERDDVDALEGVCHFFRERAEKREGAERLLKMONORGSGRALFQDLQPSQDSWGT 85

Query 86 PDAMKAIVLEKSLNQALDHALGSKKADPHLCDESHLDEEKL 132

Db 61 LEAMECAFHLSINSLLEHQLAKEBGEASCATSWRATHQVK 107

RESULT 8 US-09-134-001C-4664

; Sequence 4664 Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS THERAPEUTICS

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS THERAPEUTICS

; FILE REFERENCE: CPC-007

CURRENT APPLICATION NUMBER: US/09/134, 001C

CURRENT FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: US/09/134, 001C

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055, 779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4664

LENGTH: 168

TYPE: PRT

ORGANISM: *Staphylococcus epidermidis*

US-09-134-001C-4664

Query Match 17.0%; Score 146; DB 3; Length 168;
 Best Local Similarity 25.5%; Pred. No. 1e-0; Mismatches 67; Indels 16; Gaps 5;
 Matches 42; Conservative 40; MisMatches 67; Indels 16; Gaps 5;

Y 2 STEVAANVLNLVLYRASYTTLISLGPFYFDDVDALEGVCFFRELAEKREGAREGLRKMQ 61
 Y 5 SKELLALNQNMQYFFAHAYMAMAYACDE--SYDGFANFYFOAKERPHGKKIYD 62

b 62 QNQRGGRALFQDLOKPSQDEWGTFDDAKMAAVLVEKSLNQALDLHALGSKKADPHLCDF 121
 b 63 INDRGEHAIFDTIKAP-KVFSSILETFKDSLQAERDVTOFRYNLSELARNNDKDYATISF 121

Y 122 LESHLDEEVLKLIMKGDHNTIQRLVSKAGLE---YLFER 161
 b 122 L-NWFLDEQVEEESTPETHIDYLTR----IGDCTLYYE 158

b ; ORGANISM: Corynebacterium glutamicum
 ; US-09-602-777A-362

RESULT 9
 Sequence 362; Application US/09602777A
 GENERAL INFORMATION:
 Patent No. 6831165
 APPLICANT: Pompejus, Markus
 APPLICANT: Schroder, Hartwig
 APPLICANT: Zelder, Oskar
 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
 TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
 FILE REFERENCE: BGI-128CP
 CURRENT APPLICATION NUMBER: US/09/602-777A

PRIOR APPLICATION NUMBER: US 60/141031
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: DE 19931636.8
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19932125.6
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932126.4
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932127.2
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932128.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932129.9
 PRIOR FILING DATE: 1999-07-19
 PRIOR APPLICATION NUMBER: DE 19932226.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932920.6
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932922.2
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932924.9
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932928.1
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932930.3
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932933.8
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932935.4
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19932973.7
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19933002.6
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19933003.4
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19933005.0
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19933006.9
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19941378.9

Query Match 10.9%; Score 94; DB 4; Length 162;
 Best Local Similarity 22.1%; Pred. No. 0.034; Mismatches 72; Indels 10; Gaps 4;
 Matches 34; Conservative 38; MisMatches 72; Indels 10; Gaps 4;

QY 4 EVEAANVLNLVLYRASYTTLISLGPFYFDDVDALEGVCFFRELAEKREGARELKKMQ 63
 Db 6 KIASAFNNQVTAELRASMVYIQLSVL-DDLGTCMRDWKKAQKEELERHQKFAOHLI 63

QY 64 QRGGRALFQDLOKPSQDEWGTFDDAKMAAVLVEKSLNQALDLHALGSKKADPHLCDF 120
 Db 64 DRDYPHOIGDIAPKLDVTSIA-EFAEASLAHEQKQSGLIRELAQIQAEDYDSRALID 122

QY 121 FLESHLDEEVKLIMKGDHNTIQRLVSKAGL 154
 Db 123 W---PLNEQIEBEATVGEGIDRURAGDGSGL 152

RESULT 10
 Sequence 14335; Application US/09489039A
 ; Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gaby Breton et. al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709_200401
 CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 14335
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-14335

Query Match 10.2%; Score 88; DB 4; Length 175;
 Best Local Similarity 22.4%; Pred. No. 0.16; Mismatches 86; Indels 10; Gaps 4;
 Matches 36; Conservative 29; MisMatches 86; Indels 10; Gaps 4;

QY 3 TEVEAANVLNLVLYRASYTTLISLGPFYFDDVDALEGVCFFRELAEKREGARELKKMQ 62
 Db 14 TDMIKLNQNMQYFFAHAYMAMAYACDE--SYDGFANFYFOAKERPHGKKIYD 71

QY 63 NQGRGGRALFQDLOKPSQDEWGTFDDAKMAAVLVEKSLNQALDLHALGSKKADPHLCDFL 122
 Db 72 TDTGSLPRIMAIASPPA-EYASLDELPROTEHEOLITOKINELAHAMMTSQDYPFNFL 130

QY 123 ESHFLD--EYVVLKIMKGDHNTIQRLVSKAGLYLFER 161
 Db 131 QWYVABQHEEVKLFSVIDLT----LAGKSGBLGYFDK 166

RESULT 11
 US-09-300-909-18
 ; Sequence 18, Application US/09300909

; Patent No. 6306580
; GENERAL INFORMATION:
; APPLICANT: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
; TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 01-MAY-1998
; APPLICATION NUMBER: US/09/300, 909
; FILING DATE: 01-MAY-1998
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 644 amino acids
; TYPE: amino acid
; STRANDBNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-300-909-18

RESULT 12

Query Match 9.7%; Score 83.5; DB 3; Length 644;
Best Local Similarity 21.9%; Pred. No. 3; Mismatches 28; Conservative 22; Mismatches 55; Indels 23; Gaps 2;

Qy 60 RKNONQRGRGRLFQDQKPSQDWGTPDAMMKAIIVLEKSINQALDLIHALGSKKADPHLC 119
Db 304 KURSOTCALWNPRTAMSNISDVQGTIPEWIRLTVLQHSFNDFNIDFOLSEMVQAWDNLT 363
Qy 120 D-----PLESPLDEEVKLKQMGDEILNINORLVIKSKAGIGEYL 159
Db 364 DDDSDIAVYYAQLADSNSNAAPLKNS--NSOKIVKDQGNGCRHYCKAEKKRMSIGQWIQ 420
Qy 160 ERLTLKHD 167
Db 421 SRCEKTM 428

RESULT 13

Query Match 9.5%; Score 82; DB 4; length 998;
Best Local Similarity 24.1%; Pred. No. 7.9; Mismatches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

Qy 12 LVNLYLVRASYTILSGLF---YFDRDVA-----LEGVCFFPRELAEEREGAER 57
Db 328 LHLYQLOQUESTRAIPPKEGLPSKQVAFSTQHPRELSEIQRVYHLYAVEAK---- 381
Qy 58 LKKNONQRGRGRLFQDQKPSQDWGTPDAMMKAIIVLEKSINQALDLI--ALGSKKA 114
Db 382 -----SAFIHDTONPLKAWETYLATLADA-----SQPTISNHRLAIGWKSE 424
Qy 115 DPFLCDPLESPLDEEVKLK 135
Db 425 DPFLCDPLESPLDEEVKLK 445

US-09-198-452A-841

RESULT 14

Query Match 9.5%; Score 82; DB 4; length 998;
Best Local Similarity 24.1%; Pred. No. 7.9; Mismatches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

Qy 129 --BEUKLIKKONGDHNTI 144
Db 128 QHEESEKLENSILDKLAMV 145

RESULT 14

Query Match 9.5%; Score 82; DB 4; length 998;
Best Local Similarity 24.1%; Pred. No. 7.9; Mismatches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

Qy 129 --BEUKLIKKONGDHNTI 144
Db 128 QHEESEKLENSILDKLAMV 145

GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198-452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO: 841
LENGTH: 998
TYPE: PRT
ORGANISM: Chlamydia pneumoniae

US-09-198-452A-841

GENERAL INFORMATION:
APPLICANT: Stephon, Richard
TITLE OF INVENTION: PROTEUS MIRABILIS
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438, 185A
CURRENT FILING DATE: 2002-03-13
PRIORITY NUMBER: US 60/108, 279
PRIORITY FILING DATE: 1998-11-12
PRIORITY APPLICATION NUMBER: US 60/128, 606
PRIORITY FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: RatSeq for Windows Version 3.0
SEQ ID NO: 793
LENGTH: 998
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: Cpn0791
US-09-438-185A-793

Query Match 9.5%; Score 82; DB 4; length 998;
Best Local Similarity 24.1%; Pred. No. 7.9; Mismatches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

Qy 9 VWRVLUVLRASTYTLSLGPFEDRDPVALGVCHFRBLAEKFREGAERLQIWNQNGRR 68
Db 11 LNEQINLNFYPSANLYLOMWSAC--DDKGCFDGAALKHRSREMEMHORLFDLSDTGAM 68

Query Match 9.5%; Score 82; DB 4; length 998;
Best Local Similarity 24.1%; Pred. No. 7.9; Mismatches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

Qy 69 ALFQDQIQLPSQDWGTPDAMKAIVLKSLNQALDLIHALGSKKADPHLCDFLESHLD 128

Matches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;
 Qy 12 LVNLVLRASYVYLSTCP--YFDRDVA-----LEGVCFRELAEKREGAER 57
 Db 328 LILHYQIQUESTRAIFKEGILFSKEQAFSTQHPRBLESEIQRVYHLAYEAK---- 381
 . Qy 58 LILKMONQRGGRALFQDQIKSSQDEWGTPDAMKAATVLEKSINQALLDH---ALGSKKA 114
 Db 382 -----SAFIHDTONPLKANEYTTLADA-----SOPTISNHLALGWKSE 424
 Qy 115 DPHLCDFPLESHFLDEEVKLK 135
 Db 425 DPHSLVSLVTHFVEEVENIR 445

RESULT 15
 US-09-300-909-19
 ; Sequence 19, Application US/09300909
 Patent No. 6306580
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
 NUMBER OF SEQUENCES: 27
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/300,909
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/083,942
 FILING DATE: 01-MAY-1998
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 629 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-300-909-19

Query Match 9.4%; Score 80.5; DB 3; Length 629;
 Best Local Similarity 21.6%; Pred. No. 6.1;
 Matches 22; Conservative 20; Mismatches 37; Indels 23; Gaps 2;
 Qy 80 DEWGETPDAKKATVLEKSKINQALLDHAGS-----KADPHIC 119
 Db 311 DVYGETPEWIRBQTVLQHSFNDDTFDLSQMVQWAVNDVMDSEIAKYQAQLADSDSNAC 370
 Qy 120 DPFLSHPFLDEEVKLKMDHILNIQRLVSKAGIGBYLER 161
 Db 371 AFLKS---NSQAKIVKDGGTMCRRHYKRAEKHQMSMGQWIKSR 409

Search completed: August 22, 2005, 09:07:09
 Job time : 44 SECs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: August 22, 2005, 09:06:18 ; Search time 1065 Seconds

(Without alignments) 61.404 Million cell updates/sec

Title: US-10-617-955-2-COPY

Perfect score: 860

Sequence: 1 YSTEVEAVNLVNLVYLRS.....VKSAGLGEYLFERILTKHD 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications At: *

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2: /cgnd_6/prodata/1/pubpaal/PCT NEW PUB,pep:*

3: /cgnd_6/prodata/1/pubpaal/US06 NEW PUB,pep:*

4: /cgnd_6/prodata/1/pubpaal/US06 NEW PUB,pep:*

5: /cgnd_6/prodata/1/pubpaal/PCT NEW PUB,pep:*

6: /cgnd_6/prodata/1/pubpaal/PCT NEW PUB,pep:*

7: /cgnd_6/prodata/1/pubpaal/US08 NEW PUB,pep:*

8: /cgnd_6/prodata/1/pubpaal/US09B NEW PUB,pep:*

9: /cgnd_6/prodata/1/pubpaal/US09C NEW PUB,pep:*

10: /cgnd_6/prodata/1/pubpaal/US09C NEW PUB,pep:*

11: /cgnd_6/prodata/1/pubpaal/US10A NEW PUB,pep:*

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14: /cgnd_6/prodata/1/pubpaal/US10C NEW PUB,pep:*

15: /cgnd_6/prodata/1/pubpaal/US10D NEW PUB,pep:*

16: /cgnd_6/prodata/1/pubpaal/US11A NEW PUB,pep:*

17: /cgnd_6/prodata/1/pubpaal/US11A NEW PUB,pep:*

18: /cgnd_6/prodata/1/pubpaal/US11A NEW PUB,pep:*

19: /cgnd_6/prodata/1/pubpaal/US11A NEW PUB,pep:*

20: /cgnd_6/prodata/1/pubpaal/US11A NEW PUB,pep:*

21: /cgnd_6/prodata/1/pubpaal/US60 NEW PUB,pep:*

22: /cgnd_6/prodata/1/pubpaal/US60 NEW PUB,pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	850	98.8	167	16	US-10-617-955-4
2	849	98.7	167	16	US-10-617-955-2
3	839	97.6	175	15	US-10-042-865-174
4	799	92.9	167	14	US-10-142-938B2
5	799	87.9	175	10	US-09-919-333
6	756	87.9	175	15	US-10-435-66-4
7	756	87.9	175	15	US-10-262-445-56
8	756	87.9	175	16	US-10-734-664-128
9	756	87.9	175	16	US-10-684-742-14
10	756	87.9	175	17	US-10-489-740-14
11	756	87.9	254	15	US-10-104-047-3198

ALIGNMENTS

RESULT	1	US-10-617-955-4
		; Sequence 4, Application US/10617955
		; Publication No. US20040142164A1
		GENERAL INFORMATION:
		APPLICANT: Matsushita Electric Industrial Co., Ltd.
		APPLICANT: Yamashita, Ichiro
		TITLE OF INVENTION: FINE PARTICLE FILM AND PRODUCING METHOD OF THE SAME
		FILE REFERENCE: 051352-0039
		CURRENT APPLICATION NUMBER: US10-617-955
		CURRENT FILING DATE: 2003-07-14
		PRIOR APPLICATION NUMBER: PCT/JP2002/11954
		PRIOR FILING DATE: 2002-11-07
		PRIOR APPLICATION NUMBER: 2001-343526
		PRIOR FILING DATE: 2001-11-08
		NUMBER OF SEQ ID NOS: 4
		SOFTWARE: Patentin version 3.2
		SEQ ID NO: 4
		LENGTH: 167
		TYPE: PRT
		ORGANISM: Artificial Sequence
		FEATURE: OTHER INFORMATION: Recombinant Liver of Apoferritin of Equus cebellus
		US-10-617-955-4
		Query Match Similarity 98.8%; Score 850; DB 16; Length 167;
		Best Local Similarity 98.8%; Pred. No. 2.99-81; Indels 0; Gaps 0;
		Matches 165; Conservative 1; Mismatches 1; Insertions 0; Deletions 0;
Qy	1	YSTEVEAVNLVNLVYLRSAYTYSLGFYFDRDVVALGEGCHFFRELAEEKREGAEILK
Db	1	YSTEVEAVNLVNLVYLRSAYTYSLGFYFDRDVVALGEGCHFFRELAEEKREGAEILK
OY	61	MQNORGGRALFQDLOKPSQDEWGTPDAMGAIVLEKSINQALDLHALGSKKADPHLC 120

RESULT 2
US-10-617-955-2
; Sequence 2, Application US/10617955
; Publication No. US20040142164A1

GENERAL INFORMATION:

APPLICANT: Matsushita Electric Industrial Co., Ltd.
TITLE OF INVENTION: FINE PARTICLE FILM AND PRODUCING METHOD OF THE SAME
FILE REFERENCE: 061352-0039
CURRENT APPLICATION NUMBER: US/10-617, 955
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: PCT/JP02/11954
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 2001-343526
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 167
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Recombinant Liver Apoferritin of Equus cabellus
; US-10-617-955-2

Query Match 98.7%; Score 849; DB 16; Length 167;
Best Local Similarity 98.8%; Prod. No. 3.6e-81; Mismatches 1; Indels 0; Gaps 0;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLVLKRSAYTTLISLGFYFRDDVALGEVCHFRELAEEKREGAEERLKK 60
Db 1 YSTEVEAVNLVNLVLKRSAYTTLISLGFYFRDDVALGEVCHFRELAEEKREGAEERLKK 60

QY 61 MONQRGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINOALLDHALGSKADPHLCD 120
Db 61 MONQRGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINOALLDHALGSKADPHLCD 120

QY 121 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 167
Db 121 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 167

QY 121 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 167
Db 121 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 167

QY 129 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 175
Db 129 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 175

RESULT 3
US-10-042-865-174
; Sequence 174, Application US/10042865
; Publication No. US20040029216A1

GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
APPLICANT: Shemoy, Suresh G
APPLICANT: Sprek, Kimberly
APPLICANT: Zhong, Mei
APPLICANT: Gangoli, Esha A
APPLICANT: Burgess, Catherine E
APPLICANT: Paturajan, Meera
APPLICANT: Vernet, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Tchernov, Velizar T
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ference L
APPLICANT: Grose, William M
APPLICANT: Alsobrook II, John P

Query Match 98.7%; Score 849; DB 16; Length 175;
Best Local Similarity 97.6%; Prod. No. 4.4e-80; Mismatches 2; Indels 0; Gaps 0;
Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLVLKRSAYTTLISLGFYFRDDVALGEVCHFRELAEEKREGAEERLKK 60
Db 9 YSTEVEAVNLVNLVLKRSAYTTLISLGFYFRDDVALGEVCHFRELAEEKREGAEERLKK 68

QY 61 MONQRGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINOALLDHALGSKADPHLCD 120
Db 69 MONQRGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINOALLDHALGSKADPHLCD 128

QY 121 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 167
Db 129 FLESHFLDEVKLIKMDHMTNIORLVGSQAGLGEYLFERLTIKHD 175

RESULT 4
US-10-142-838B-2
; Sequence 2, Application US/10142838B
; Publication No. US20030124741A1

GENERAL INFORMATION:

APPLICANT: Matsushita Electric Industrial Co., Ltd.
TITLE OF INVENTION: Recombinant cage-like protein, Method for producing the same, Precious metal-recombinant cage-like protein complex, Method for producing the same and recombinant DNA
FILE REFERENCE: Apoferritin DNA PRT
CURRENT APPLICATION NUMBER: US/10/142,838B
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: JP/P2001-142983
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 167
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Recombinant Liver Apoferritin

OTHER INFORMATION: of Equus cabellus
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (46)
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (50)
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (53)
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (56)
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (57)
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (120)
 FEATURE:
 NAME/KEY: MUTAGEN
 LOCATION: (123)

US-10-142-838B-2

Query Match 92.9%; Score 799; DB 14; Length 167;
 Best Local Similarity 93.4%; Pred. No. 6.8e-76; Mismatches 5; Indels 0; Gaps 0;
 Matches 156; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLTYRASITYLISGFYFDRDVALEGVCHFFBLAEERKREGERLK 60
 Db 1 YSTEVEAVNLVNLTYRASITYLISGFYFDRDVALEGVCHFFBLAEERKREGERLK 60

QY 61 MONORGGRALFDQLOPKSDQEWGTTDAMKAIVLEKSINQALDIHALGSKKADPHCD 120
 Db 61 MONORGGRALFDQLOPKSDQEWGTTDAMKAIVLEKSINQALDIHALGSKAQADPHCS 120

QY 121 FLESHLDEEVKLKIKMGDHILNTORLVLQSGYLFERLTKHD 167
 Db 121 FLESHLDEEVKLKIKMGDHILNTORLVLQSGYLFERLTKHD 167

RESULT 5
 Sequence 333, Application US/09919039
 Publication No. US20030108871A1
 GENERAL INFORMATION:
 APPLICANT: Kaser, Matthew R.
 TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 FILE REFERENCE: PA-0035 US
 CURRENT APPLICATION NUMBER: US/09/919,039
 CURRENT FILING DATE: 2002-09-09
 PRIOR APPLICATION NUMBER: 60/222,113
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 401
 SOFTWARE: PERL Program
 SEQ ID NO 333
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc feature
 OTHER INFORMATION: Incyte ID No. US20030108871A1 4005778CD1
 US-09-919-039-33

Query Match 87.9%; Score 756; DB 10; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71; Mismatches 11; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLTYRASITYLISGFYFDRDVALEGVCHFFBLAEERKREGERLK 60
 Db 9 YSTEVEAVNLVNLTYRASITYLISGFYFDRDVALEGVCHFFBLAEERKREGERLK 68

QY 61 MONORGGRALFDQLOPKSDQEWGTTDAMKAIVLEKSINQALDIHALGSKKADPHCD 120
 Db 69 MONORGGRALFDQLOPKSDQEWGTTDAMKAIVLEKSINQALDIHALGSARTDPHCD 128

QY 121 FLESHLDEEVKLKIKMGDHILNTORLVLQSGYLFERLTKHD 167
 Db 129 FLESHLDEEVKLKIKMGDHILNTLHRGGPEAGLGYLFERLTKHD 175

RESULT 6
 Sequence 4, Application US/10435666
 Publication No. US2004000601A1
 GENERAL INFORMATION:
 APPLICANT: CARTER, Daniel C.
 TITLE OF INVENTION: FERRITIN FUSION PROTBINS FOR USE IN VACCINES AND OTHER APPLICATIONS
 FILE REFERENCE: P07624WO0/BAS
 CURRENT APPLICATION NUMBER: US/10/435,666
 CURRENT FILING DATE: 2003-05-12
 PRIOR APPLICATION NUMBER: 60/5379,145
 PRIOR FILING DATE: 2002-05-10
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 4
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-435-666-4

Query Match 87.9%; Score 756; DB 15; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71; Mismatches 12; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLTYRASITYLISGFYFDRDVALEGVCHFFBLAEERKREGERLK 60
 Db 9 YSTEVEAVNLVNLTYRASITYLISGFYFDRDVALEGVCHFFBLAEERKREGERLK 68

QY 61 MONORGGRALFDQLOPKSDQEWGTTDAMKAIVLEKSINQALDIHALGSKKADPHCD 120
 Db 69 MONORGGRALFDQLOPKSDQEWGTTDAMKAIVLEKSINQALDIHALGSARTDPHCD 128

QY 121 FLESHLDEEVKLKIKMGDHILNTORLVLQSGYLFERLTKHD 167
 Db 129 FLESHLDEEVKLKIKMGDHILNTLHRGGPEAGLGYLFERLTKHD 175

RESULT 7
 Sequence 56, Application US/10262445
 Publication No. US2004014058A1
 GENERAL INFORMATION:
 APPLICANT: Albrook II, John
 APPLICANT: Burgess, Catherine
 APPLICANT: Catterton, Elina
 APPLICANT: Chant, John
 APPLICANT: Chaudhuri, Amitabha
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Giot, Loic
 APPLICANT: Gorman, Linda
 APPLICANT: Guo, Xiaojia
 APPLICANT: Kekuda, Ramesh
 APPLICANT: Mezei, Peter
 APPLICANT: Millet, Isabelle
 APPLICANT: Ooi, Chean Eng
 APPLICANT: Patturajan, Meera
 APPLICANT: Rieger, Daniel
 APPLICANT: Spyrek, Kimberly
 APPLICANT: Taupier Jr., Raymond J.
 APPLICANT: Zerhusen, Bryan
 APPLICANT: Zhong, Haihong
 APPLICANT: Zheng, Mei
 TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
 TITLE OF INVENTION: THE SAME

FILE REFERENCE: 21402-462D
 CURRENT APPLICATION NUMBER: US/10/262,445
 CURRENT FILING DATE: 2002-10-01
 PRIOR APPLICATION NUMBER: 60/327,454
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 60/327,917
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/328,029
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/328,056
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/328,849
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/329,414
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 60/330,142
 PRIOR FILING DATE: 2001-10-17
 PRIOR APPLICATION NUMBER: 60/341,058
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: 60/343,629
 PRIOR FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 60/349,575
 PRIOR FILING DATE: 2001-10-29
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 133
 SOFTWARE: CuraseqList version 0.1
 SEQ ID NO 56
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-262-445-56

RESULT 9
 Query Match 87.9%; Score 756; DB 15; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71; Mismatches 11; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAAVNVLVNLVYLRASTYVTLIGYFDRDVAGLEGVSHFRELAEEKRGERYLKK 60
 Db 9 YSTDYEAVAVNSVLNVLYQASVTYLSIGYFDRDVAGLEGVSHFRELAEKRGERYLKK 68

Qy 61 MONORGGRALFDQLOKPSQDEWGKTPDAMKAIVLVEKSINQALLDHALGSKKADPHLCD 120
 Db 69 MQNQRGGRALFDQDQKPAEDEWGKTPDAMKAIVLVEKSINQALLDHALGSKKADPHLCD 128

Qy 121 FLESHFLDBEVKLTKMDHNTIQRLVSKAGLGEYLFRERUTKHD 167
 Db 69 MONORGGRALFDQLOKPSQDEWGKTPDAMKAIVLVEKSINQALLDHALGSKKADPHLCD 128

Db 129 FLETHFLDBEVKLTKMDHNTIQRLVSKAGLGEYLFRERUTKHD 175

US-10-734-564-128

; Sequence 128 Application US/10734564
 ; Publication No. US20040115728A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Christopher C Burgess et al
 ; TITLE OF INVENTION: Detection Methods Using TIMPL
 ; FILE REFERENCE: 16572012
 ; CURRENT APPLICATION NUMBER: US/10/734,564
 ; CURRENT FILING DATE: 2003-12-12
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 128
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-734-564-128

Query Match 87.9%; Score 756; DB 16; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAAVNVLVNLVYLRASTYVTLIGYFDRDVAGLEGVSHFRELAEEKRGERYLKK 60
 US-10-684-742-14

RESULT 10
 Query Match 87.9%; Score 756; DB 16; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71; Mismatches 11; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAAVNVLVNLVYLRASTYVTLIGYFDRDVAGLEGVSHFRELAEEKRGERYLKK 60
 Db 9 YSTDYEAVAVNSVLNVLYQASVTYLSIGYFDRDVAGLEGVSHFRELAEKRGERYLKK 68

Qy 61 MONORGGRALFDQLOKPSQDEWGKTPDAMKAIVLVEKSINQALLDHALGSKKADPHLCD 120
 Db 69 MQNQRGGRALFDQDQKPAEDEWGKTPDAMKAIVLVEKSINQALLDHALGSKKADPHLCD 128

Qy 121 FLESHFLDBEVKLTKMDHNTIQRLVSKAGLGEYLFRERUTKHD 167
 Db 69 MONORGGRALFDQLOKPSQDEWGKTPDAMKAIVLVEKSINQALLDHALGSKKADPHLCD 128

Db 129 FLETHFLDBEVKLTKMDHNTIQRLVSKAGLGEYLFRERUTKHD 175

US-10-419-740-144

RESULT 10
 Query Match 87.9%; Score 756; DB 17; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

RESULT 11
 US-10-104-047-3198
 ; Sequence 3198, Application US/10104047
 ; Publication No. US20030236392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3198
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-104-047-3198

Query Match 87.9%; Score 756; DB 15; Length 254;
 Best Local Similarity 86.2%; Pred. No. 4e-71; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVLRASYTISLGFYFRRDVALEGVCHPFRBLAEKREGAERLLK 60
 Db 88 YSTDVERAANVLVNLVLRASYTISLGFYFRRDVALEGVCHPFRBLAEKREGAERLLK 147

Qy 61 MONORGGRALFDQLOQPSQDEWGKTPDAMCAVILEKSINQALLDHALGSKKADPHLCD 120
 Db 148 MONORGGRALFDQLOQPSQDEWGKTPDAMCAVILEKSINQALLDHALGSARTDPHLC 207

Qy 121 FLESHFLDEEVKLKINGDHNTNOLRUVKSAGLGEYLFERLTKHID 167
 Db 208 FLETHFLDEEVKLKINGDHNTNOLRUVKSAGLGEYLFERLTKHID 254

RESULT 12
 US-10-042-865-171
 ; Sequence 171, Application US/10042865
 ; Publication No. US20040029216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pedigaru, Muralidhara
 ; APPLICANT: Li, Li
 ; APPLICANT: Zerhuen, Bryan D
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Shenoj, Suresh G
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Gangoli, Esha A
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Patterson, Meera
 ; APPLICANT: Vernet, Corine A.M
 ; APPLICANT: Taylor, Sarah
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Miller, Charles E
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Boldog, Ference L
 ; APPLICANT: Grossie, William M
 ; APPLICANT: Alsobrook II, John P

Query Match 87.9%; Score 756; DB 15; Length 254;
 Best Local Similarity 86.2%; Pred. No. 4e-71; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVLRASYTISLGFYFRRDVALEGVCHPFRBLAEKREGAERLLK 60
 Db 88 YSTDVERAANVLVNLVLRASYTISLGFYFRRDVALEGVCHPFRBLAEKREGAERLLK 147

Qy 61 MONORGGRALFDQLOQPSQDEWGKTPDAMCAVILEKSINQALLDHALGSKKADPHLCD 120
 Db 148 MONORGGRALFDQLOQPSQDEWGKTPDAMCAVILEKSINQALLDHALGSARTDPHLC 207

Qy 121 FLESHFLDEEVKLKINGDHNTNOLRUVKSAGLGEYLFERLTKHID 167
 Db 208 FLETHFLDEEVKLKINGDHNTNOLRUVKSAGLGEYLFERLTKHID 254

RESULT 13
 US-10-732-923-5089
 ; Sequence 5089, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 5089
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-10-732-923-5089

Query Match 85.8%; Score 738; DB 17; Length 175;
 Best Local Similarity 85.6%; Pred. No. 1.9e-69; Indels 0; Gaps 0;
 Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLKRASTYTLISLGFYFDRDVALLGVCHFRELAEEKREGAERLKK 60
 9 VSTEVEAVNLVNLKRASTYTLISLGFYFDRDVALLGVCHFRELAEEKREGAERLKK 68
 Db 61 MONQRGRALFODVKPSQDWGTPDAMKAVALVEKSINQALDLHALGSKCADPHLCID 120
 69 MONQRGRALFODVKPSQDWGKTNAMEALALKNQALDLHALGSAKTDPHLCD 128
 QY 121 FLESHFLDEVKLIKKGDHNTIQRLVSKAGLGEYLPERLTIKHD 167
 Db 129 FLENHFLDEVKLIKKGDHNTIQRLVSKAGLGEYLPERLTIKHD 175

RESULT 14
 US-10-042-865-172
 ; Sequence 172, Application US/10042865
 ; Publication No. US2004002916A1
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Li, Li
 APPLICANT: Zethusen, Bryan D
 APPLICANT: Casman, Stacie J
 APPLICANT: Shenvy, Suresh G
 APPLICANT: Spyrek, Kimberly
 APPLICANT: Zhong, Mei
 APPLICANT: Gangoli, Esha A
 APPLICANT: Burgess, Catherine E
 APPLICANT: Patterajan, Meera
 APPLICANT: Vernet, Corine A.M
 APPLICANT: Taylor, Sarah
 APPLICANT: Tchernev, Velizar T
 APPLICANT: Miller, Charles E
 APPLICANT: Guo, Xiaojia
 APPLICANT: Boldog, Ference L
 APPLICANT: Grose, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Gerlach, Valerie L
 APPLICANT: Edlinger, Shlomit R
 APPLICANT: Rothenberg, Mark E
 APPLICANT: Ellerman, Karen
 APPLICANT: Macbougall, John
 APPLICANT: Malvankar, Uriel M
 APPLICANT: Millet, Isabelle
 APPLICANT: Peyman, John
 APPLICANT: Smithson, Glenna
 APPLICANT: Gunther, Erik
 APPLICANT: Stone, David
 TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
 TITLE OF INVENTION: Using the Same
 FILE REFERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865
 CURRENT FILING DATE: 2003-05-17
 CURRENT APPLICATION NUMBER: US/10/042,865
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/260,417
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/260,831
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: 60/272,338
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: 60/274,876
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/284,704
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 264
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 172
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Cavia porcellus

RESULT 15
 US-10-042-865-173
 ; Sequence 173, Application US/10042865
 ; Publication No. US2004002916A1
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Li, Li
 APPLICANT: Zethusen, Bryan D
 APPLICANT: Casman, Stacie J
 APPLICANT: Shenvy, Suresh G
 APPLICANT: Spyrek, Kimberly
 APPLICANT: Zhong, Mei
 APPLICANT: Gangoli, Esha A
 APPLICANT: Burgess, Catherine E
 APPLICANT: Patterajan, Meera
 APPLICANT: Vernet, Corine A.M
 APPLICANT: Taylor, Sarah
 APPLICANT: Tchernev, Velizar T
 APPLICANT: Miller, Charles E
 APPLICANT: Guo, Xiaojia
 APPLICANT: Boldog, Ference L
 APPLICANT: Grose, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Gerlach, Valerie L
 APPLICANT: Edlinger, Shlomit R
 APPLICANT: Rothenberg, Mark E
 APPLICANT: Ellerman, Karen
 APPLICANT: Macbougall, John
 APPLICANT: Malvankar, Uriel M
 APPLICANT: Millet, Isabelle
 APPLICANT: Peyman, John
 APPLICANT: Smithson, Glenna
 APPLICANT: Gunther, Erik
 APPLICANT: Stone, David
 TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
 TITLE OF INVENTION: Using the Same
 FILE REFERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865
 CURRENT FILING DATE: 2002-03-17
 PRIOR APPLICATION NUMBER: 60/260,417
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/260,831
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: 60/272,338
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: 60/274,876
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/284,704
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 264
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 173
 LENGTH: 183
 TYPE: PRT
 ORGANISM: Rattus norvegicus

RESULT 16
 US-10-042-865-174
 ; Sequence 174, Application US/10042865
 ; Publication No. US2004002916A1
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Li, Li
 APPLICANT: Zethusen, Bryan D
 APPLICANT: Casman, Stacie J
 APPLICANT: Shenvy, Suresh G
 APPLICANT: Spyrek, Kimberly
 APPLICANT: Zhong, Mei
 APPLICANT: Gangoli, Esha A
 APPLICANT: Burgess, Catherine E
 APPLICANT: Patterajan, Meera
 APPLICANT: Vernet, Corine A.M
 APPLICANT: Taylor, Sarah
 APPLICANT: Tchernev, Velizar T
 APPLICANT: Miller, Charles E
 APPLICANT: Guo, Xiaojia
 APPLICANT: Boldog, Ference L
 APPLICANT: Grose, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Gerlach, Valerie L
 APPLICANT: Edlinger, Shlomit R
 APPLICANT: Rothenberg, Mark E
 APPLICANT: Ellerman, Karen
 APPLICANT: Macbougall, John
 APPLICANT: Malvankar, Uriel M
 APPLICANT: Millet, Isabelle
 APPLICANT: Peyman, John
 APPLICANT: Smithson, Glenna
 APPLICANT: Gunther, Erik
 APPLICANT: Stone, David
 TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
 TITLE OF INVENTION: Using the Same
 FILE REFERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865
 CURRENT FILING DATE: 2002-03-17
 PRIOR APPLICATION NUMBER: 60/260,417
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/260,831
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: 60/272,338
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: 60/274,876
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/284,704
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 264
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 174
 LENGTH: 183
 TYPE: PRT
 ORGANISM: Rattus norvegicus

RESULT 17
 US-10-042-865-175
 ; Sequence 175, Application US/10042865
 ; Publication No. US2004002916A1
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Li, Li
 APPLICANT: Zethusen, Bryan D
 APPLICANT: Casman, Stacie J
 APPLICANT: Shenvy, Suresh G
 APPLICANT: Spyrek, Kimberly
 APPLICANT: Zhong, Mei
 APPLICANT: Gangoli, Esha A
 APPLICANT: Burgess, Catherine E
 APPLICANT: Patterajan, Meera
 APPLICANT: Vernet, Corine A.M
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 APPLICANT: Tchernev, Velizar T
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 APPLICANT: Millet, Isabelle
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 APPLICANT: Smithson, Glenna
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 TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
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 PRIOR APPLICATION NUMBER: 60/284,704
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 264
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 175
 LENGTH: 183
 TYPE: PRT
 ORGANISM: Rattus norvegicus

Query Match 85.0%; Score 731; DB 15; Length 175;
 Best Local Similarity 84.4%; Pred. No. 1.1e-68;

Best local similarity 81.7%; Pred. No. 1.4e-68; Matches 143; Conservative 15; Mismatches 9; Indels 8; Gaps 1;
Qy 1 YSTEVEAAVNRLVNLTYLRASTYIISLGFYRDRDVALEGVCHFFRELAEERKREGERLIK 60
Db 9 YSTEVEAAVNRLVNLVNLRASTYIISLGFFDRDVALEGVCHFFRELAEERKREGERLIK 68
Qy 61 MQNQRGGRALFQDQLQPSQDEWGTPDAMCAIVLKSNQALUDHALGSKKADPHLC 120
Db 69 LQNERGGRALFQDVKPSQEWGKTEAMKALEKNQALUDHALGSAQADPHLC 128
Qy 121 FLESHPFLDEEVKLKKGMDITNIQ-----LVSKAGLGEVLFERILKHD 167
Db 129 FLESHPFLDKVKLIKKGMDITNIQRLRRWQGFQPAQTVGAQASIGEYLFERILKHD 183

Search completed: August 22, 2005, 09:28:43
Job time : 1066 secs

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CC ROM, and magnetic disks. The present sequence is a protein sequence for horse liver apoferritin, used to illustrate the invention

XX

SQ Sequence 167 AA;

Query Match Best Local Similarity 98.8%; Score 850; DB 6; Length 167; Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSTEVEAANVLNLYRASVTYLISLGFWFDRDDVDALEGVCHFRELAEEKREGAERLKK 60

Db 1 YSTEVEAANVLNLYRASVTYLISLGFWFDRDDVDALEGVCHFRELAEEKREGAERLKK 60

QY 61 MONORGGRALFQDLOQPSQDEWGTTPDAMKAATVLEKSLNQALLDHALGSKKADPHLCD 120

Db 61 MONORGGRALFQDLOQPSQDEWGTTPDAMKAATVLEKSLNQALLDHALGSKKADPHLCD 120

QY 121 FLESHFLDREVKLJIKKMGDHITNQRLVSKAGLGEYLFRERLTIKHD 167

Db 121 FLESHFLDREVKLJIKKMGDHITNQRLVSKAGLGEYLFRERLTIKHD 167

RESULT 2 ABP56247 standard; protein; 167 AA.

ID ABR56247 standard; protein; 167 AA.

XX

AC ABR56247;

XX

DT 20-NOV-2003 (first entry)

XX

DE Horse liver apoferritin #1.

XX

KW Horse; liver apoferitin.

XX

OS Equus caballus.

FH Key Location/Qualifiers

FT Misc-difference 112..113 /note= "Encoded by AGG AGG"

XX

WO2003040025-A1.

XX

PD 15-MAY-2003.

FT 07-NOV-2002; 2002WO-JP011594.

XX

PR 08-NOV-2001; 2001JP-00343526.

XX

PA (MATU) MATSUSHITA ELECTRIC IND CO LTD.

XX

PA (MATU) MATSUSHITA ELECTRIC IND CO LTD.

PI Yamashita I,

XX

DR WPI; 2003-150217/15.

DR N-PSDB; ABV77632.

XX

PT Film used in analysis of protein crystal structure by electron microscopy, and in manufacturing float gates and magnetic disks contains micrograins of proteins aligned regularly at high density.

PS Disclosure; Page 41; 47pp; Japanese.

XX

The present invention relates to a micrograin film, comprising a substrate and micrograins made of proteins that are regularly arranged on the surface of the substrate in the plane direction parallel to the surface. The film is useful in analysis of protein crystal structure by electron microscopy, and in manufacturing float gates of E2P-ROM or E2P-CC ROM, and magnetic disks. The present sequence is a protein sequence for horse liver apoferritin, used to illustrate the invention

SQ Sequence 167 AA;

Query Match Best Local Similarity 98.8%; Score 849; DB 6; Length 167;

Best Local Similarity 98.8%; Pred. No. 4.8e-80;

Best Local Similarity 93.4%; Pred. No. 7.7e-75;

Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSTEVEAANVLNLYRASVTYLISLGFWFDRDDVDALEGVCHFRELAEEKREGAERLKK 60

Db 1 YSTEVEAANVLNLYRASVTYLISLGFWFDRDDVDALEGVCHFRELAEEKREGAERLKK 60

QY 61 MONORGGRALFQDLOQPSQDEWGTTPDAMKAATVLEKSLNQALLDHALGSKKADPHLCD 120

Db 61 MONORGGRALFQDLOQPSQDEWGTTPDAMKAATVLEKSLNQALLDHALGSKKADPHLCD 120

RESULT 3 ABP57965 standard; protein; 167 AA.

ID ABP57965 standard; protein; 167 AA.

XX

AC ABP57965;

XX

DT 06-MAR-2003 (first entry)

XX

DE Horse liver apoferritin recombinant protein.

XX

KW Horse; apoferretin; cage-like protein; precious metal; semiconductor;

XX

OS Equus caballus.

FH Key Location/Qualifiers

FT Misc-difference 73 /note= "Encoded by ACC"

FT Misc-difference 75 /note= "Encoded by TCC"

XX

EP-262489-A1.

XX

PD 04-DEC-2002.

XX

PF 13-MAY-2002; 2002EP-00010688.

XX

PR 14-MAY-2001; 2001JP-00142933.

XX

PA (MATU) MATSUSHITA ELECTRIC IND CO LTD.

XX

Yamashita I;

XX

DR WPI; 2003-150217/15.

DR N-PSDB; ABV77632.

XX

PT Novel recombinant cage-like protein for producing semiconductors, has a holding portion, present in internal portion of protein for holding precious metal particle and connected to outside by tunnel-like channel.

XX

PS Disclosure; Page 16; 30pp; English.

XX

The invention relates to a novel recombinant cage-like protein, produced by a gene recombination technique. The cage-like protein is useful for holding a precious metal to form a complex which is useful for producing semiconductors. The metal particle-protein complexes are useful in bioelectronics. The invention has the advantage that the precious metal particle having a uniform size of nanometer order can be formed in the holding portion of the recombinant cage-like protein, so that minute dot bodies made of precious metal having excellent chemical stability is produced efficiently. The present sequence represents the protein product of the recombinant DNA of liver apoferitin of Equus caballus (horse) of the invention

XX

Sequence 167 AA;

Query Match Best Local Similarity 92.9%; Score 799; DB 6; Length 167;

Best Local Similarity 93.4%; Pred. No. 7.7e-75;

PS Claim 2; Page 141; 253pp; English.
 XX
 CC The invention describes an isolated polypeptide comprising any of 33 90-
 CC 1273 amino acid sequences (I) given in the specification or its mature
 CC form, a sequence that is at least 95 % identical to (I), or a sequence
 CC comprising one or more conservative substitutions in the amino acid
 sequence of (I). The polypeptide is useful for preparing a composition
 CC for treating or preventing e.g. cancer. This is the amino acid sequence
 CC of a novel human NOV protein
 XX
 SQ Sequence 175 AA:

Query Match 87.9%; Score 756; DB 6; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.4e-70; Mismatches 12; Indels 0; Gaps 0;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 1 YSTEVEAVANVLNVLYRASVTYLGLGPFRRDVALLEGNSHFFRELAEKREGERLLK 60
 Db 9 YSTDVEAVNLSLVNLQASVTLISLGYFDRDVALLEGNSHFFRELAEKREGERLLK 68
 QY 61 MONORGGRALFQDLOKPSQDWGTPDAMKAIVAKVSKLNAQALLDHIALGSKKADPHLC 120
 Db 69 MONORGGRALFQDIIKKPAEDWGKTPDAMKAAMTLEKCKLNQALLDHALGSAARTDPHLC 128
 QY 121 FLESHFLDEEVKLTKKGMDHNTIQRLVKSAGLGYLFERLTIKHD 167
 Db 129 FLETHFLDEEVKLTKKGMDHNTIQRLVKSAGLGYLFERLTIKHD 175

RESULT 6

ADG42356

ID ADG42356 standard; peptide; 175 AA.

AC

ADG42356;

XX

DT 26-FEB-2004 (first entry)

XX

DE Ferritin L chain for HIV tat peptide-ferritin L chain fusion protein.

XX

DE anti-HIV; virucide; vaccine; gene therapy; ferritin; fusion protein; polymeric assembly; AIDS; SARS; oxygen transport; blood substitute; KW image contrast agent; metal chelating agent; gelling agents; protein purification platform.

KW Homo sapiens.

OS

XX

PN WO2003094849-A2.

XX

PD 20-NOV-2003.

XX

PP 12-MAY-2003; 2003WO-US014617.

XX

PR 10-MAY-2002; 2002US-0379145P.

XX

PA (NEWC-) NEW CENTURY PHARM INC.

XX

PI Carter DC, Li CQ;

XX

WPI; 2003-903936/82.

XX

DR N-PSDB; ADE77167.

XX

PT Composition comprising several cDNAs that are differentially expressed in PT treated human C3A liver cell cultures, useful for treating liver disorders.

XX

PS Claim 1; SEQ ID NO 333; 41pp; English.

XX

The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the

CC or in other applications including oxygen transport and the therapeutic delivery of drugs and other therapeutic agents, or as blood substitutes, image contrast agents, metal chelating agents, gelling agents, protein purification platforms, and therapeutic receptor-binding proteins. In an example of the invention, a peptide from the HIV Tat protein is fused to the N-terminus of the ferritin L chain via a 6 GLY spacer. This peptide represents the ferritin L chain which is fused to the HIV Tat peptide.

XX
 SQ Sequence 175 AA;

Query Match 87.9%; Score 756; DB 7; Length 175;

Best Local Similarity 86.2%; Pred. No. 2.4e-70; Mismatches 12; Indels 0; Gaps 0;

Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAVANVLNVLYRASVTYLGLGPFRRDVALLEGNSHFFRELAEKREGERLLK 60

Db 9 YSTDVEAVNLSLVNLQASVTLISLGYFDRDVALLEGNSHFFRELAEKREGERLLK 68

QY 61 MONORGGRALFQDLOKPSQDWGTPDAMKAIVAKVSKLNAQALLDHIALGSKKADPHLC 120

Db 69 MONORGGRALFQDIIKKPAEDWGKTPDAMKAAMTLEKCKLNQALLDHALGSAARTDPHLC 128

QY 121 FLESHFLDEEVKLTKKGMDHNTIQRLVKSAGLGYLFERLTIKHD 167

Db 129 FLETHFLDEEVKLTKKGMDHNTIQRLVKSAGLGYLFERLTIKHD 175

RESULT 7

ADE77168

ID AD77168 standard; protein; 175 AA.

XX

AC ADE77168;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human protein expressed in a liver disorder #85.

XX

DE Human protein expressed in a liver disorder #85.

XX

DE human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; KW tumour; liver; inflammatory disorder; immune response; disorder; KW high-throughput screening; differential gene expression; gene therapy.

XX

OS Homo sapiens.

XX

US2003108871-A1.

XX

PN 12-JUN-2003.

XX

PD 30-JUL-2001; 2001US-00919039.

XX

PR 28-JUL-2000; 2000US-0222113P.

XX

PA (KASE/) KASER M R.

XX

Kaser MR;

XX

PI WPI; 2004-031227/03.

XX

DR N-PSDB; ADE77167.

XX

PT Composition comprising several cDNAs that are differentially expressed in PT treated human C3A liver cell cultures, useful for treating liver disorders.

XX

PS Claim 1; SEQ ID NO 333; 41pp; English.

XX

The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the

CC protein selected from a ferritin protein fused at the C-terminus or at the N-terminus with a protein or peptide capable of being fused to ferritin without interfering with the polymeric assembly of the resulting fusion protein. The fusion proteins are useful in the development of new ferritin fusion proteins in which ferritin is fused with a protein capable of being fused to ferritin without interfering with polymeric assembly of resulting fusion protein, useful as human or veterinary vaccines and therapeutics.

XX Example 3; SEQ ID NO 4; 52pp; English.

The invention relates to a ferritin fusion protein comprising a fusion protein selected from a ferritin protein fused at the C-terminus or at the N-terminus with a protein or peptide capable of being fused to ferritin without interfering with the polymeric assembly of the resulting fusion protein. The fusion proteins are useful for a novel human NOV protein

XX

CC human and veterinary vaccines and therapeutics against e.g. AIDS or SARS,

DT	129	FLETHFLDEEVKLIKKGMDHLTNLHLGLGPEAGLGIVYPERLTLKHD	175
XX			
DB		Tumour-associated antigenic target (TAT) polypeptide PRO71085, SEQ:5563.	
XX			
KW		Tumour-associated antigenic target; TAT; human; overexpression; cancer;	
KW		tumour; diagnosis; cell proliferative disorder; breast cancer; liver cancer;	
KW		colorectal cancer; lung cancer; ovarian cancer; bladder cancer; pancreatic cancer;	
KW		central nervous system cancer; cervical cancer; melanoma; leukaemia; hybridisation probe;	
KW		chromosome identification; chromosome mapping; gene mapping;	
KW		gene therapy; cytostatic.	
OS		Homo sapiens.	
XX			
PN		WO2004030615-A2.	
XX			
PD	15-APR-2004.		
XX			
PP	29-SEP-2003; 2003WO-US028547.		
XX			
PR	02-OCT-2002; 2002US-0414971P.		
XX			
PA	(GETH) GEMENTECH INC.		
XX			
PT	Wu TD, Zhang Z, Zhou Y;		
XX			
PT	WPI; 2004-347921/32.		
DR	N-PSDB; ACN40653.		
XX			
PT	New tumor-associated antigenic target polypeptides and nucleic acids,		
PT	useful in preparing a medicament for treating or detecting a		
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or		
PT	prostate cancer or tumor.		
PS	Claim 12; SEQ ID NO 5563; 7273pp; English.		
XX			
CC	The invention relates to human tumour-associated antigenic target (TAT)		
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are		
CC	overexpressed in cancer tissues compared to normal tissues, and may thus		
CC	serve as effective targets for the diagnosis and treatment of cancer in		
CC	mammals. The invention also relates to nucleic acid and polypeptide		
CC	sequences at least 80% identical to the TAT nucleic acids and		
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic		
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic		
CC	acid; an antibody which binds to a TAT polypeptide; fusion proteins comprising a		
CC	TAT polypeptide; and methods and compositions for the treatment or		
CC	diagnosis of cancer in mammals. TAT Polypeptides, nucleic acids,		
CC	antibodies, antagonists, binding molecules and compositions are useful		
CC	for diagnosing or treating a cell proliferative disorder associated with		
CC	increased TAT expression, particularly cancers such as breast cancer,		
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder		
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central		
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be		
CC	used as hybridisation probes, in chromosome and gene mapping, in		
CC	chromosome identification and in gene therapy. The present sequence		
CC	represents a TAT polypeptide of the invention		
SQ	Sequence 175 AA;		
Query Match	87.9%; Score 756; DB 8; Length 175;		
Best Local Similarity	86.2%; Pred. No. 2; 4e-70;		
Matches	144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;		
Oy	1 YSTEVEAANVLNLVLYRASYYTISLGLYFDRDVDALEGVCFPRELAEEKRGGAERILK 60		
Db	9 YSTIDEAVAVNLNVLYLQSYTISLGLYFIDRDVALGEVSIFRFELABEKEGYELIK 68		
Oy	61 MONORGGRALFQDQLQPKSDEWGFTPDAMKAATVLEKSINQALDLHALGSKKADPLCD 120		
Db	69 MONORGGRALFQDQLQPKSDEWGFTPDAMKAAMALEKLNQALDLHALGSKARTDPHLCD 128		
SQ	Sequence 254 AA;		
Query Match	87.9%; Score 756; DB 7; Length 254;		

Best Local Similarity 86.2%; Pred. No. 4e-70; Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYRASYTTLISGFYFRDVALEGCFHFFRELAERKREGAERLKK 60
Db 88 YSTDVERAANVLVNLVYRASYTTLISGFYFRDVALEGCFHFFRELAERKREGAERLKK 147

Qy 61 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINQALLDHALGSKADPHLCD 120
Db 148 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINQALLDHALGSKADPHLCD 207

Qy 121 FLESHTFLDEEVKLTKIKMGDHITNIORLUVKSKAGLGFLYFLERLTKH 167
Db 208 FLETIHFDEEVKLTKIKMGDHITNLHRLGGPAGLGFLYFLERLTKH 254

RESULT 13
ADQ82746 ADQ82746 standard; protein; 362 AA.

XX ADQ82746;
XX DT 09-SEP-2004 (first entry)
XX DE Recombinant human ferritin protein.
XX KW human; ferritin protein.
XX OS Homo sapiens.
XX PN KR2004007992-A.
XX PD 28-JAN-2004.
XX FF 11-JUL-2002; 2002KR-00040497.
XX PR 11-JUL-2002; 2002KR-00040497.

XX PA (BIOP-) BIOPROGEN CO LTD.
PI Ham MS, Jung BH, Kim SU, Lee EG, Lee JW;
XX DR N-PSDB; ADQ82747.

PT New recombinant human ferritin proteins and production method of them.
XX PS Claim 8; SEQ ID NO 11; 27PP; Korean.

XX The invention comprises the amino acid and coding sequences of a recombinant human ferritin protein, the invention also comprises a production method for the recombinant human ferritin protein. The present sequence represents the recombinant human ferritin protein of the invention.

XX SQ Sequence 362 AA:

Query Match 87.9%; Score 756; DB 8; Length 362;
Best Local Similarity 86.2%; Pred. No. 6.2e-70; Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYRASYTTLISGFYFRDVALEGCFHFFRELAERKREGAERLKK 60
Db 196 YSTDVERAANVLVNLVYRASYTTLISGFYFRDVALEGCFHFFRELAERKREGAERLKK 131

Qy 61 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINQALLDHALGSKADPHLCD 120
Db 256 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINQALLDHALGSKADPHLCD 315

Qy 121 FLESHTFLDEEVKLTKIKMGDHITNIORLUVKSKAGLGFLYFLERLTKH 167
Db 316 FLETIHFDEEVKLTKIKMGDHITNLHRLGGPAGLGFLYFLERLTKH 362

RESULT 14
AAU2923 AAU2923 standard; protein; 238 AA.

XX AAU2923;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #414.
XX KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; hematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US008656.
XX PR 18-APR-2000; 2000US-00552929.
XX PR 26-JAN-2001; 2001US-0070160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
XX PS Claim 20; Page 210; 755pp; English.

CC The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for CC determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are also useful for CC identifying agents (agonists and antagonists) that bind to them. Cells CC expressing the proteins are useful for identifying a therapeutic agent CC for use in treatment of a pathology related to aberrant expression or CC physiological interactions of the polypeptide. Vectors comprising the CC nucleic acids encoding the polypeptides and cells genetically engineered CC to express them are also useful for producing the proteins. The proteins CC are useful in genetic vaccination, testing and therapy, and can be used CC as nutritional supplements. They may be used to increase stem cell CC proliferation, to regulate haemopoiesis, and in bone, cartilage, tendon CC and/or nerve tissue growth or regeneration; immune suppression and/or CC stimulation; as anti-inflammatory agents; and in treatment of leukemias. CC AU2951-AAU3304 represent the amino acid sequences of novel human CC secreted proteins of the invention

XX SQ Sequence 238 AA;

Query Match 87.6%; Score 753; DB 4; Length 238;
Best Local Similarity 85.6%; Pred. No. 7.5e-70; Matches 143; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 YSTEVEAVNLVNLVYRASYTTLISGFYFRDVALEGCFHFFRELAERKREGAERLKK 60
Db 72 YSTDVERAANVLVNLVYRASYTTLISGFYFRDVALEGCFHFFRELAERKREGAERLKK 131

Qy 61 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINQALLDHALGSKADPHLCD 120
Db 132 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSINQALLDHALGSKADPHLCD 191

Qy 121 FLESHTFLDEEVKLTKIKMGDHITNIORLUVKSKAGLGFLYFLERLTKH 167
Db 192 FLETIHFDEEVKLTKIKMGDHITNLHRLGGPAGLGFLYFLERLTKH 238

RESULT 15
 ADO60419
 ID ADO60419 standard; protein; 175 AA.
 XX
 AC ADO60419;
 DT 26-AUG-2004 (first entry)
 DE Human ferritin light chain to increase B lymphocyte proliferation.
 XX
 KW B lymphocyte proliferation; differentiation; maturation; ferritin;
 KW diagnosis; HIV infection; lymphoma.
 XX
 OS Homo sapiens.
 XX
 PN WO2004045561-A2.
 XX
 PD 03-JUN-2004.
 XX
 PP 20-NOV-2003; 2003WO-US037593.
 XX
 PR 20-NOV-2002; 2002US0427754P.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Stevenson M, Swigler S;
 XX
 DR WPI; 2004-431807/40.
 XX
 PT Inducing B cell proliferation, differentiation or maturation for treating
 PT HIV infection or cancer, comprises administering ferritin or a compound
 PT that increases ferritin expression or activity to the B cell or its
 PT precursor cell.
 XX
 PS Example 1; SEQ ID NO 1; 86pp; English.
 XX
 CC The invention relates to a method of increasing at least one of B
 CC lymphocyte proliferation, differentiation or maturation, by administering
 CC ferritin or a compound that increases ferritin expression or activity to
 CC a B lymphocyte or a B lymphocyte precursor cell in an amount to increase
 CC B lymphocyte proliferation, differentiation or maturation. The methods
 CC are useful for modulating B lymphocyte proliferation, differentiation or
 CC maturation, or for identifying compounds that modulate ferritin
 CC expression or activity. These may be used for treating or diagnosing HIV
 CC infection or lymphoma. This sequence corresponds to the human ferritin
 CC light chain protein used in the method of the invention.
 XX
 SQ Sequence 175 AA;

Query Match 86.3%; Score 742; DB 8; Length 175;
 Best Local Similarity 85.0%; Pred. No. 7e-69;
 Matches 142; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Oy 1 YSTEVEAVRNLYVNLYRASYTTLISLGYPFRDVALGEVGCFPRELAEEKREGAERLLK 60
 Oy 9 YSTDVEAVNVLNVNLQLRSYYTSLISGFYFRDVALGEVGSHFRELABEERKREGERLLK 68
 Oy 61 MONORGERALFDQLOQKSQDGUTTPDAMKAIVLERSINQALDHALGSKKADPHLCD 120
 Db 69 MONORGVALFDQLOQKSQDGUTTPDAMKAIVLERSINQALDHALGSKKADPHLCD 128
 Oy 121 FLESHPFDEEVKLKKGMDHLTNIQRLVKSAGLGELVFERITLKHD 167
 Db 129 FLETHPFDDEEVKLKKGMDHLTNIQRLVKSAGLGELVFERITLKHD 175

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:17 ; Search time 172 Seconds
(Without alignment)
497.193 Million cell updates/sec

Title: US-10-617-955-2-COPY

Perfect score: 860

Sequence: 1 YSTEVEALAVNRLVNLVYRAS.....VKSAGLGEVLFERLTIKHD 167

Scoring table: BLOSUM62

Gapop 10 0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	839	97.6	174	FRII_HORSE
2	756	87.9	174	1 FRII_HUMAN
3	756	87.9	241	Q7Z2W1
4	752	87.4	2	Q1BFT7
5	750	87.2	175	2 Q96AU9
6	748	87.0	175	Q86CU0
7	747	86.9	175	2 Q8WU07
8	745	86.6	175	2 Q86W19
9	745	86.6	175	2 Q9JKMB
10	738	85.8	174	1 FRII_BOVIN
11	738	85.8	174	1 FRII_RABIT
12	731	85.0	175	2 Q8YK6
13	728	84.7	183	2 Q8PT71
14	726	84.4	182	1 FRII_RAT
15	726	84.4	182	1 FRII_MOUSE
16	721	83.8	183	2 Q9CPX4
17	716	83.3	183	2 Q9CPX4
18	712	82.8	182	1 FRII_MOUSE
19	712	82.8	183	2 Q6GWW0
20	709	82.4	191	2 Q8S4P3
21	673	78.3	160	2 Q96J87
22	595.5	69.2	1310	2 Q7TP54
23	538	62.5	178	2 Q624N0
24	536	62.3	176	2 Q6P8C6
25	535	62.2	176	1 FRII_RANCA
26	534	62.1	178	2 Q7ZWW3
27	532	61.9	173	2 Q6DP5
28	61.6	177	1 FRII_XENLA	
29	529	61.5	177	2 Q801J5
30	528	61.4	176	2 Q6P8B7
31	61.2	177	2 Q6PG53	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1	FRIL_HORSE	STANDARD:	PRT:	174 AA.
ID	FRIL_HORSE			
AC	P02791; P02791;			
DT	21-JUL-1986 (Rel. 01, Created) 01-NOV-1995 (Rel. 32, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DR	Ferritin light chain (Ferritin L subunit).			
GN	Name=FRTL;			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
RN	[1]; NCBI_TaxID=9796;			
RN	RN			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	RC			
RC	MEDLINE=82027739; PubMed=7026284; DOI=10.1016/0014-5793(81)90121-S;			
RA	Heubter-Sprante M., Crichton R.R.;			
RA	"Amino acid sequence of horse spleen apo ferritin.";			
RA	FEBS Lett. 129:322-327(1981).			
RA	[3]			
RA	SEQUENCE.			
RA	TISSUE=Spleen;			
RA	MEDLINE=82027739; PubMed=7026284; DOI=10.1016/0014-5793(81)90121-S;			
RA	Mathijssen J.M., Crichton R.R.;			
RA	"Amino acid sequence of horse liver ferritin.";			
RA	S. Afr. J. Sci. 80:424-426(1984).			
RA	[4]			
RA	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).			
RA	MEDLINE=81052459; PubMed=7433529;			
RA	Clegg G.A., Stansfield R.F.D., Harrison P.E., Harrison P.M.;			
RA	"Helix packing and subunit conformation in horse spleen apo ferritin.";			
RA	Nature 288:298-300(1980).			
RA	[5]			
RA	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).			
RA	PubMed=15299370;			
RA	RX			
RA	Piecikoux Y., Yariv J., Gallois B., Dautant A., Courbessie C.,			
RA	D'Estaintot B.L.;			
RA	"A crystallographic study of haem binding to ferritin.";			
RA	Acta Crystallogr. D 50:739-743(1994).			
RA	[6]			
RA	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).			
RA	MEDLINE=97303059; PubMed=1159481; DOI=10.1006/jmbi.1997.0970;			
RA	Hempstead P.D., Yewdall S.J., Ernie A.R., Lawson D.M., Arrymiuuk P.J., Rice D.W., Ford G.C., Harrison P.M.;			
RA	"Comparison of the three-dimensional structures of recombinant human H and horse L ferritins at high resolution.";			

RL J. Mol. Biol. 268:424-448(1997).
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and
 CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited.
 CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
 CC chain and H (heavy) chain. The major chain can be light or heavy,
 CC depending on the species and tissue type.
 CC -!- MISCELLANEOUS: In horse spleen the light chain is the major chain.
 CC -!- SIMILARITY: Belongs to the ferritin family.
 CC -!- SIMILARITY: Contains 1 ferritin-like dirron domain.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; D14523; BAA3396.1; -.
 DR PIR; S36118; FRHOL.
 DR PDB; 1AFW; X-ray; @=1-174.
 DR PDB; 1DAB; X-ray; @=1-174.
 DR PDB; 1GWC; X-ray; A=1-174.
 DR PDB; 1HRS; X-ray; @=1-174.
 DR PDB; 1IER; X-ray; @=1-174.
 DR PDB; 1IERS; X-ray; A/B/C/D/E/F=1-174.
 DR PROSITE; PS00240; Ferritin; 1.
 DR PROSITE; PS00240; FERRITIN_2; 1.
 DR PROSITE; PS00240; FERRITIN_LIKE; 1.
 DR KW 3D-structure; Acetylation; Direct protein sequencing; Iron;
 DR KW Ion storage; Metal-binding.
 FT INIT_MET 0 0
 FT DOMAIN 6 155 Ferritin-like diiron.
 FT DOMAIN 53 60 Catalytic site for iron oxidation.
 FT MOD_RES 1 1 N-acetylserine.
 FT METAL 53 53 Iron (Potential).
 FT METAL 56 56 Iron (Potential).
 FT METAL 57 57 Iron (Potential).
 FT METAL 60 60 Iron (Potential).
 FT METAL 63 63 Iron (Potential).
 FT CONFLICT 93 93 P -> L (in Ref. 2 and 3).
 FT CONFLICT 135 137 DDE -> NEQ (in Ref. 3).
 FT HELIX 10 36
 FT TURN 37 38
 FT TURN 40 42
 FT HELIX 45 72
 FT TURN 73 73
 FT HELIX 92 120
 FT TURN 121 121
 FT HELIX 123 132
 FT TURN 133 133
 FT HELIX 134 157
 FT HELIX 159 169
 FT TURN 170 170
 SQ SEQUENCE 174 AA; 19830 MW; AE039CA1BD046D4F CRC64;

Query Match 97.6%; Score 839; DB 1; Length 174;
 Best Local Similarity 97.6%; Pred. No. 7.5e-62; DB 1;
 Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSTEVEAARNLVLVNLVYRASYTYLSIGFYEDRDVALEGCVHFRRELSEKREGERLIK 60
 Db 8 YSTEVEAARNLVLVNLVYRASYTYLSIGFYEDRDVALEGCVHFRRELSEKREGERLIK 67

RESULT 2
 FRIL_HUMAN STANDARD:
 ID FRIL_HUMAN PRT: 174 AA.
 AC P02752; Q9BTZ8;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ferritin light chain (Ferritin L subunit).
 GN Name=FRIL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606; [1]
 RN RR
 RN MEDLINE-85216457; PubMed=3154330;
 RA Santoro C., Marone M., Ferrone M., Costanzo F., Colombo M.,
 RA Minganti C., Cortese R., Silengo L.;
 RT "Cloning of the gene coding for human L apoferritin.";
 RL Nucleic Acids Res. 14:2863-2876(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86176772; PubMed=3154570;
 RA Dorner M.H., Salfeld J., Will H., Leibold E.A., Vass J.K., Munro H.N.;
 RT "Structure of human ferritin light subunit messenger RNA: comparison
 with heavy subunit message and functional implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3133-3143(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RN MEDLINE-8600223; PubMed=31540162;
 RA Boyd D., Vecoli C., Belcher D.M., Jain S.K., Drysdale J.W.;
 RT "Structural and functional relationships of human ferritin H and L
 chains deduced from cDNA clones.";
 RL J. Biol. Chem. 260:11755-11761(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=brain, Skin, and Urinary bladder;
 RX MEDLINE-22382257; PubMed=112477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Reinbold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuller G.D.,
 RA Altschul S.F., Zeeberg B.H., Buetow K.H., Schaefer C.R., Blat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton B., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Boutefaud G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 32-174 FROM N.A.
 RX MEDLINE-8706341; PubMed=3123856;
 RA Chou C.-C., Gatti R.A., Fuller M.L., Concannon P., Wong A., Chada S.,
 RA Davis R.C., Salter W.A.;
 RT "Structure and expression of ferritin genes in a human promyelocytic

RT	cell line that differentiates in vitro.";
RL	Mol. Cell. Biol. 6:566-573(1986).
RN	[6]
RP	SEQUENCE OF 1-35 AND 40-174.
RC	TISSUE=Liver;
RX	Medline=80108507; PubMed=6653779; DOI=10.1016/0074-5733(83)80037-4;
RA	Addison J M., Pittton J.B., Lewis W.G., May K., Harrison P.M.;
RT	"The amino acid sequence of human liver apoferritin.";
RL	FEMS Lett. 164:139-144(1983).
[7]	
RP	SEQUENCE OF 83-89 AND 144-154.
RC	TISSUE=Placenta;
RX	PubMed=8706699;
RA	Vladimirov S.N., Ivanov A.V., Karpova G.G., Musolyamov A.K.,
RA	Egorov T.A., Thiede B., Wittmann-Liebold B., Otto A.;
RT	Characterization of the human small-ribosomal-subunit proteins by N-terminal and internal sequencing, and mass spectrometry.";
RL	J. Biochem. 239:1441-149(1996).
CC	Bur. J. Biochem. 239:1441-149(1996).
CC	-I- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron core is deposited.
CC	-I- MISCELLANEOUS: There are two types of ferritin subunits: L (light) chain and H (heavy) chain. The major chain can be light or heavy, depending on the species and tissue type.
CC	-I- SIMILARITY: Belongs to the ferritin family.
CC	-I- SIMILARITY: Contains 1 ferritin-like diiron domain.
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DR	EMBL; M1147; AAA52439.1; .
DR	EMBL; M10119; AAA35831.1; .
DR	EMBL; M12938; AAA52440.1; .
DR	EMBL; BC002991; AAH02991.2; .
DR	EMBL; BC00245; AAH0245.1; .
DR	EMBL; BC008439; AAH0439.1; .
DR	EMBL; BC016346; AAH16346.1; .
DR	EMBL; BC016354; AAH16354.1; .
DR	EMBL; BC016990; AAH16990.1; .
DR	EMBL; BC058820; AAH58820.1; .
DR	EMBL; X03742; CAA27383.1; .
DR	EMBL; X03743; CAA27383.1; .
DR	EMBL; X03743; CAA27384.1; .
DR	PIR; B23920; PRH01.
DR	HSSP; P239391; I1B33.
DR	GeneW; HGNC:3999; FTL.
DR	H-Invis; HRX0015310; .
DR	MIN; 134790; .
DR	GO; GO:0009043; C:ferritin complex; TAS.
DR	GO; GO:0005506; F:iron ion binding; TAS.
DR	GO; GO:006379; F:iron ion homeostasis; TAS.
DR	InterPro; IPR01519; Ferritin.
DR	InterPro; IPR00831; Ferritin_Dps.
DR	InterPro; IPR00831; Ferritin_Dps.
DR	InterPro; IPR00940; Ferritin_like.
DR	InterPro; IPR00940; Ferritin_like.
DR	Pfam; PF00210; Ferritin.
DR	ProDom; PD000971; Ferritin.
DR	Prosite; PS00540; FERITIN_1; 1.
DR	Prosite; PS00204; FERITIN_2; 1.
DR	Prosite; PS00905; FERITIN_LIKE; 1.
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DR	Metal-binding.
FT	INIT_MET
FT	DOMAIN
FT	MOD_RES
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Q7Z2W1	Query Match 87.9%; Score 756; DB 1; Length 174;
Q7Z2W1	Best Local Similarity 86.2%; Pred. No. 5. 9e-55;
Q7Z2W1	Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
AC	YSTDYEAIVNLVNLQLQSATYISLGFYFDRDVQEVSHFFRELAEKKREGYERLLK 67
DB	1 YSTEVEAVNLVNLQLQSATYISLGFYFDRDVQEVSHFFRELAEKKREGYERLLK 60
QY	61 MNQRGGRALFQDLOKPSQDEWGTTPDAMGAIVLEKSNQALDLHALGSKADPHLD 120
DB	68 MQNRGGRALFQDIKPDEWGKTPDAMGAIVLEKSNQALDLHALGSARTPHLC 127
QY	121 FLESHTLDEEVKLKENGDHILNTORLVLKSKAGLGBYLFERLTKD 167
DB	128 FLBTHFLDEEVKLKNGDHILNLHRLLGGPEAGLGBYLFRLTKD 174
SO	SEQUENCE 174 AA; 19898 MW; 870B4B3B6C9E9F2 CRC64;
FT	METAL 53
FT	METAL 56
FT	METAL 57
FT	METAL 60
FT	METAL 63
FT	CONFLICT 53
FT	CONFLICT 86
FT	CONFLICT 88
FT	CONFLICT 101
FT	CONFLICT 153
FT	CONFLICT 174
FT	E -> Q (in Ref. 5);
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FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);
FT	W -> P (in Ref. 5);
FT	W -> R (in Ref. 5);
FT	W -> S (in Ref. 5);
FT	W -> T (in Ref. 5);
FT	W -> V (in Ref. 5);
FT	W -> Y (in Ref. 5);
FT	W -> F (in Ref. 5);
FT	W -> G (in Ref. 5);
FT	W -> H (in Ref. 5);
FT	W -> I (in Ref. 5);
FT	W -> K (in Ref. 5);
FT	W -> L (in Ref. 5);
FT	W -> M (in Ref. 5);
FT	W -> N (in Ref. 5);

Query Match 87.2%; Score 750; DB 2; Length 175;
 Best Local Similarity 85.6%; Pred. No. 1. 9e-54; DR InterPro; IPR009078; Ferritin/RR like.
 Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0; DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009340; ferritin_like.
 DR Pfam; PF00210; Ferritin_1.
 DR ProDom; PD000371; Ferritin_1.
 DR PROSITE; PS00540; FERRITIN_1.
 DR PROSITE; PS00504; FERRITIN_2.
 DR PROSITE; PS50505; FERRITIN_Like.
 DR Iron; Iron storage; Metal-Binding.
 KW Sequence; 175 AA; 20039 MW; ODB9915724EB0BC2 CRC64;

Qy 1 YSTEVEAVNLVNLVYLASYTLYSISGFYFPRDVDALEGVSFHFRALAEERGEGARLLK 60
 DR 9 YSTDVEAVNLVNLVYLASYTLYSISGFYFPRDVDALEGVSFHFRALAEERGEGARLLK 68
 DR 61 MONORGGRALFODLOKPSQDGNTTPDAMKAIVLVEKSLNQALLDHALGSKKADPHLC 120
 DR 69 MONORGGRALFODIKKPAEDWGKTPDAMKAALMELKLNQALLDHALGSAARTDPRLCD 128

Db Qy 121 FLESHFDEEVKLKIKGDHUTNIQLVSKAGLGEYLFERLTLD 167
 DR 129 FLETHFDEEVKLKIKGDHUTNLHRLLGGPAGLGEYLFERLTLD 175

RESULT 6

Q96CU0 PRELIMINARY; PRT; 175 AA.
 ID Q96CU0 PRELIMINARY; PRT; 175 AA.
 AC Q96CU0; 01-DEC-2001 (TREMBlre. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlre. 19, Last sequence update)
 DE Ferritin, light polypeptide.
 GN Name=FML;
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN Q8WU07
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=2388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg K.H., Schaeffer C.C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15, 000 full-length human
 and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [1]
 SEQUENCE FROM N.A.

RESULT 7

Q8WU07 PRELIMINARY; PRT; 175 AA.
 ID Q8WU07
 AC 08WU07;
 DT 01-MAR-2002 (TREMBlre. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBlre. 26, Last annotation update)
 DE Ferritin, light polypeptide.
 GN Name=FML;
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN Q8WU07
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=2288257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaeffer C.C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15, 000 full-length human
 and mouse cDNA Sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 SEQUENCE FROM N.A.

TISSUE=Brain;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron core is deposited (BY similarity).

-I- SIMILARITY: Belongs to the ferritin family.

-I- SIMILARITY: Contains 1 ferritin-like domain.

EMBL: BC001928; ARH1928.1; - .

HSSP: P23931; IUD3.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0005679; P:iron ion homeostasis; IEA.

DR GO; GO:0006866; P:iron ion transport; IEA.

DR InterPro; IPR001519; Ferritin.

DR InterPro; IPR009078; Ferritin/RR like.

DR InterPro; IPR008331; Ferritin_Dps.

DR InterPro; IPR009340; ferritin_like.

DR Pfam; PF00210; Ferritin_1.

DR ProDom; PD000371; Ferritin_1.

DR PROSITE; PS00540; FERRITIN_1.

DR PROSITE; PS00504; FERRITIN_2.

DR PROSITE; PS50505; FERRITIN_Like.

DR Iron; Iron storage; Metal-Binding.

KW Sequence; 175 AA; 20039 MW; ODB9915724EB0BC2 CRC64;

Query Match 87.0%; Score 748; DB 2; Length 175;
 Best Local Similarity 85.6%; Pred. No. 2. 7e-54; DR InterPro; IPR009078; Ferritin/RR like.
 Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0; DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009340; ferritin_like.

DR Pfam; PF00210; Ferritin_1.

DR ProDom; PD000371; Ferritin_1.

DR PROSITE; PS00540; FERRITIN_1.

DR PROSITE; PS00504; FERRITIN_2.

DR PROSITE; PS50505; FERRITIN_Like.

DR Iron; Iron storage; Metal-Binding.

KW Sequence; 175 AA; 20039 MW; ODB9915724EB0BC2 CRC64;

Qy 1 YSTEVEAVNLVNLVYLASYTLYSISGFYFPRDVDALEGVSFHFRALAEERGEGARLLK 60
 DR 9 YSTDVEAVNLVNLVYLASYTLYSISGFYFPRDVDALEGVSFHFRALAEERGEGARLLK 68
 DR 61 MONORGGRALFODLOKPSQDGNTTPDAMKAIVLVEKSLNQALLDHALGSKKADPHLC 120
 DR 69 MONORGGRALFODIKKPAEDWGKTPDAMKAALMELKLNQALLDHALGSAARTDPRLCD 128

Db Qy 121 FLESHFDEEVKLKIKGDHUTNIQLVSKAGLGEYLFERLTLD 167
 DR 129 FLETHFDEEVKLKIKGDHUTNLHRLLGGPAGLGEYLFERLTLD 175

CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited (By similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.

CC EMBL: BC021670; AAH21670.1; -.

DR GO: GO:005488; F:binding; IEA.

DR GO: GO:008199; F:ferric iron binding; IEA.

DR GO: GO:006879; Pi:iron ion homeostasis; IEA.

DR GO: GO:006826; Pi:iron ion transport; IEA.

DR PFam: PF00210; Ferritin; 1.

DR PFam: PF00210; Ferritin; 1.

DR PROSITE; PS00540; FERRITIN_1; 1.

DR PROSITE; PS00204; FERRITIN_2; 1.

DR PROSITE; PS50905; FERRITIN_LIKE; 1.

DR SEQUENCE 175 AA; 20062 MW; 18ADD1D0BA8C6A69 CRC64;

Query Match 86.9%; Score 747; DB 2; Length 175;
 Best Local Similarity 85.6%; Pred. No. 3.3e-54; Mismatches 13; Indels 0; Gaps 0;
 Matches 143; Conservative

QY 1 YSTEVEAVNRLVNLRYASVTYLSLGTYFDRDVALGVCHFRELAEEKREGAERLIK 60

Db 9 YSTDVEAANDSLVNLVLYASVTYLSLGTYFDRDVALGVSHFRELAEEKREGYERLIK 68

QY 61 MONORGGRALFQDLQPKSQDEWGTTPDAMKAATVLEKSLNQALDLHALGSKADPHLCD 120

Db 69 MONORGGRALFQDLQPKSQDEWGTTPDAMKAATVLEKSLNQALDLHALGSKADPHLCD 128

QY 121 FLESFLDIEEVKLLIKQMDHLTNIQOLVKSAGLBYLFLRLLHD 167

Db 129 FLETHFLDIEEVKLLIKQMDHLTNLRLLHGPPAGLBYLFERLTIKHD 175

RESULT 8
 Q86W19 PRELIMINARY; PRT; 175 AA.

ID Q9JKB8 PRELIMINARY; PRT; 175 AA.

AC Q9JKB8; AC 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DR Ferritin light chain.

DR Cavia porcellus (guinea pig).

DR Buxarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC

OS Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

DR NCBI_TaxID=10141; RN [1]

RP SEQUENCE FROM N.A. MEDLINE:20218664; PubMed=10753629; DOI=10.1006/brcr.2000.2425;

RA Cheng Q.; Gonzalez P.; Ziger J.S. Jr.; RT "High level of ferritin light chain mRNA in lens.";

RA Li X.; Ophuise J.; Tilson M.D.; RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC in a soluble, nontoxic, readily available form. The functional

CC molecule, which is composed of 24 chains, is roughly spherical and

CC contains a central cavity into which the polymeric ferric iron

CC core is deposited (By similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

RESULT 9
 Q9JKB8 PRELIMINARY; PRT; 175 AA.

ID Q9JKB8 PRELIMINARY; PRT; 175 AA.

AC Q9JKB8; AC 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DR Ferritin light chain.

DR Cavia porcellus (guinea pig).

DR Buxarvota; Metazoa; Rodentia; Hystricognathi; Caviidae; Cavia.

DR NCBI_TaxID=10141; RN [1]

RP SEQUENCE FROM N.A. MEDLINE:20218664; PubMed=10753629; DOI=10.1006/brcr.2000.2425;

RA Cheng Q.; Gonzalez P.; Ziger J.S. Jr.; RT "High level of ferritin light chain mRNA in lens.";

RA Biochem. Biophys. Res. Commun. 270:349-355 (2000).

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

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CC in a soluble, nontoxic, readily available form. The functional

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CC contains a central cavity into which the polymeric ferric iron

CC core is deposited (By similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

Q86W19 PRELIMINARY; PRT; 175 AA.

AC Q9JKB8 PRELIMINARY; PRT; 175 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DR Ferritin light chain.

DR Cavia porcellus (guinea pig).

DR Buxarvota; Metazoa; Rodentia; Hystricognathi; Caviidae; Cavia.

DR NCBI_TaxID=10141; RN [1]

RP SEQUENCE FROM N.A. MEDLINE:20218664; PubMed=10753629; DOI=10.1006/brcr.2000.2425;

RA Cheng Q.; Gonzalez P.; Ziger J.S. Jr.; RT "High level of ferritin light chain mRNA in lens.";

RA Biochem. Biophys. Res. Commun. 270:349-355 (2000).

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

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CC core is deposited (By similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

Q86W19 PRELIMINARY; PRT; 175 AA.

AC Q9JKB8 PRELIMINARY; PRT; 175 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DR Ferritin light chain.

DR Cavia porcellus (guinea pig).

DR Buxarvota; Metazoa; Rodentia; Hystricognathi; Caviidae; Cavia.

DR NCBI_TaxID=10141; RN [1]

RP SEQUENCE FROM N.A. MEDLINE:20218664; PubMed=10753629; DOI=10.1006/brcr.2000.2425;

RA Cheng Q.; Gonzalez P.; Ziger J.S. Jr.; RT "High level of ferritin light chain mRNA in lens.";

RA Biochem. Biophys. Res. Commun. 270:349-355 (2000).

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

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 CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

Q86W19 PRELIMINARY; PRT; 175 AA.

AC Q9JKB8 PRELIMINARY; PRT; 175 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DR Ferritin light chain.

DR Cavia porcellus (guinea pig).

DR Buxarvota; Metazoa; Rodentia; Hystricognathi; Caviidae; Cavia.

DR NCBI_TaxID=10141; RN [1]

RP SEQUENCE FROM N.A. MEDLINE:20218664; PubMed=10753629; DOI=10.1006/brcr.2000.2425;

RA Cheng Q.; Gonzalez P.; Ziger J.S. Jr.; RT "High level of ferritin light chain mRNA in lens.";

RA Biochem. Biophys. Res. Commun. 270:349-355 (2000).

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

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CC contains a central cavity into which the polymeric ferric iron

CC core is deposited (By similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

Q86W19 PRELIMINARY; PRT; 175 AA.

AC Q9JKB8 PRELIMINARY; PRT; 175 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DR Ferritin light chain.

DR Cavia porcellus (guinea pig).

DR Buxarvota; Metazoa; Rodentia; Hystricognathi; Caviidae; Cavia.

DR NCBI_TaxID=10141; RN [1]

RP SEQUENCE FROM N.A. MEDLINE:20218664; PubMed=10753629; DOI=10.1006/brcr.2000.2425;

RA Cheng Q.; Gonzalez P.; Ziger J.S. Jr.; RT "High level of ferritin light chain mRNA in lens.";

RA Biochem. Biophys. Res. Commun. 270:349-355 (2000).

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC in a soluble, nontoxic, readily available form. The functional

CC molecule, which is composed of 24 chains, is roughly spherical and

CC contains a central cavity into which the polymeric ferric iron

CC core is deposited (By similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

FT METAL 63 63 Iron (Potential).
 SQ SEQUENCE 174 AA; 19943 MW; B9B03050BB233BB86 CRC64;

Query Match 85.8%; Score 738; DB 1; Length 174;
 Best Local Similarity 85.6%; Pred. No. 1.8e-53;
 Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLVLYTASYTISLGFYFDRDVVALEGVCHFRELAEEKREGAERLIK
 8 YSPEVERAVNLVNLVLYTASYTISLGFYFDRDVVALAGVGHFRELAEEKREGAERLIK

Db 61 MONORGGRALFQDQKPSQDEWGTPDMKAATVLEKSLNQALDLHALGSSKKADPHLCD 60
 68 MONORGGRALFQDQKPSQDEWGKTINAMEAALAKLNQALDLHALGSAHTDPHLC 67

QY 121 FLESHFLDEVKLUKIKOMGDHTNQRLVSKAGLGLYFRLTILKH 167
 128 FLENHFLDEVKLUKIKOMGDHTNQRLSGPQASIGEYFRLTILKH 174

RESULT 12

Q9BYW6 PRELIMINARY; PRT; 175 AA.

ID Q9BYW6; PRELIMINARY; PRT; 175 AA.

AC 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DB DJ681N20.2 (Novel protein similar to ferritin, light polypeptide
 (FTL))

DE Name=dJ681N20_2;
 Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.

RP .
 RA Smith M.; (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC !- FUNCTION: Ferritin is an intracellular molecule that stores iron
 in a soluble, nontoxic, readily available form. The functional
 molecule, which is composed of 24 chains, is roughly spherical and
 contains a central cavity into which the polymeric ferric iron
 core is deposited (By similarity).

CC !- SIMILARITY: Belongs to the ferritin family.

CC !- SIMILARITY: Contains 1 ferritin-like diiron domain.

DR EMBL; ARF23098; ARF68948.1; .

DR GO; GO:0005879; F:iron ion binding; IEA.
 HSSP; P02791; 1GMG.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0008119; F:ferric iron homeostasis; IEA.

DR GO; GO:0006326; F:iron ion transport; IEA.

DR InterPro; IPR01519; Ferritin.

DR InterPro; IPR00931; Ferritin_RR_like.

DR InterPro; IPR001519; Ferritin.

DR InterPro; IPR00978; Ferritin_RR_like.

DR InterPro; IPR00833; Ferritin_Dps.

DR InterPro; IPR00940; Ferritin_Like.

DR Pfam; PF00210; Ferritin.

DR ProDom; PD000971; Ferritin; 1.

DR PROSITE; PS00540; FERRITIN_1; 1.

DR PROSITE; PS00204; FERRITIN_2; 1.

DR PROSITE; PS50905; FERRITIN_LIKE; 1.

KW Iron; Iron storage; Metal-binding.

SQ SEQUENCE 175 AA; 1994 MW; 85FDDCD31546696A CRC64;

Query Match 85.0%; Score 731; DB 2; Length 175;
 Best Local Similarity 84.3%; Pred. No. 7e-53;
 Matches 140; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLVLYTASYTISLGFYFDRDVVALEGVCHFRELAEEKREGAERLIK
 9 YSTEVEAVNLVNLVLYTASYTISLGFYFDRDVVALAGVGHFRELAEEKREGAERLIK
 68

Db 61 MONORGGRALFQDQKPSQDEWGTPDMKAATVLEKSLNQALDLHALGSSKKADPHLCD 60
 68 MONORGGRALFQDQKPSQDEWGKTINAMEAALAKLNQALDLHALGSAHTDPHLC 67

QY 121 FLESHFLDEVKLUKIKOMGDHTNQRLVSKAGLGLYFRLTILKH 167
 128 FLENHFLDEVKLUKIKOMGDHTNQRLSGPQASIGEYFRLTILKH 175

RESULT 13

Q9JKP6 PRELIMINARY; PRT; 175 AA.

ID Q9JKP6; PRELIMINARY; PRT; 175 AA.

AC 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DB 05-MAR-2004 (Tremblrel. 26, Last annotation update)

DR Ferritin light chain.

OS Cavia porcellus (guinea pig).
 OC Bovaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 NCBI_TaxID=10141;

RN [1] SEQUENCE FROM N.A.

RP .
 RA Sevoz C.; Buronfouse T.; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC !- FUNCTION: Ferritin is an intracellular molecule that stores iron
 in a soluble, nontoxic, readily available form. The functional
 molecule, which is composed of 24 chains, is roughly spherical and
 contains a central cavity into which the polymeric ferric iron
 core is deposited (By similarity).

CC !- SIMILARITY: Contains 1 ferritin-like diiron domain.

DR EMBL; ARF23098; ARF68948.1; .

DR GO; GO:0005879; F:ferric iron homeostasis; IEA.

DR GO; GO:0008119; F:iron ion transport; IEA.

DR InterPro; IPR01519; Ferritin.

DR InterPro; IPR00931; Ferritin_RR_like.

DR InterPro; IPR001519; Ferritin.

DR InterPro; IPR00978; Ferritin_RR_like.

DR InterPro; IPR00833; Ferritin_Dps.

DR InterPro; IPR00940; Ferritin_Like.

DR Pfam; PF00210; Ferritin.

DR ProDom; PD000971; Ferritin; 1.

DR PROSITE; PS00540; FERRITIN_1; 1.

DR PROSITE; PS00204; FERRITIN_2; 1.

DR PROSITE; PS50905; FERRITIN_LIKE; 1.

KW Iron; Iron storage; Metal-binding.

SQ SEQUENCE 175 AA; 1994 MW; 85FDDCD31546696A CRC64;

Query Match 85.0%; Score 731; DB 2; Length 175;
 Best Local Similarity 84.4%; Pred. No. 7e-53;
 Matches 141; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAVNLVNLVLYTASYTISLGFYFDRDVVALEGVCHFRELAEEKREGAERLIK
 9 YSTEVEAVNLVNLVLYTASYTISLGFYFDRDVVALAGVGHFRELAEEKREGAERLIK
 68

Db 61 MONORGGRALFQDQKPSQDEWGTPDMKAATVLEKSLNQALDLHALGSSKKADPHLCD 60
 68 MONORGGRALFQDQKPSQDEWGKTINAMEAALAKLNQALDLHALGSAHTDPHLC 67

QY 121 FLESHFLDEVKLUKIKOMGDHTNQRLVSKAGLGLYFRLTILKH 167
 128 FLENHFLDEVKLUKIKOMGDHTNQRLSGPQASIGEYFRLTILKH 175

RESULT 14

Q6PT1 PRELIMINARY; PRT; 183 AA.

ID Q6PT1; PRELIMINARY; PRT; 183 AA.

AC 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DB 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE	Hypothetical protein.
OS	<i>Rattus norvegicus</i> (Rat).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RP	SEQUENCE FROM N.A.
RC	TISSUE=Pituitary gland;
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,
RA	Klauner R.D., Collins F.S., Wagner L., Sheinman C.M., Schueler G.D.,
RA	Altshull S.P., Zeeberg B., Butelow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McManam K.J., Malek J.A., Gunnarsson P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzewinski M.I., Skalska S., Smailus D.B., Schnurch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Pituitary gland;
RA	Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC	-!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC	in a soluble, nontoxic, readily available form. The functional
CC	molecule, which is composed of 24 chains, is roughly spherical and
CC	contains a central cavity into which the polymeric ferric iron
CC	core is deposited (By similarity).
CC	-!- SIMILARITY: Belongs to the ferritin family.
DR	EMBL: BC01525; AAH1525.1; --.
DR	HSSP: P02791; IAEW.
CC	-!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC	in a soluble, nontoxic, readily available form. The functional
CC	molecule, which is composed of 24 chains, is roughly spherical and
CC	contains a central cavity into which the polymeric ferric iron
CC	core is deposited.
DR	EMBL: BC01519; Ferritin_RR_like.
DR	InterPro: IPR009078; Ferritin_RR_like.
DR	GO: GO:0008199; Ferric iron binding; IFA.
DR	GO: GO:0006879; Iron ion homeostasis; IFA.
DR	GO: GO:0006826; Iron ion transport; IFA.
DR	InterPro: IPR00519; Ferritin_RR_like.
DR	InterPro: IPR009078; Ferritin_RR_like.
DR	InterPro: IPR00831; Ferritin_Dps.
DR	InterPro: IPR009040; Ferritin_Like.
DR	Pfam: PF02210; Ferritin_1.
DR	ProDom: P000971; Ferritin_1.
DR	PROSITE: PS00540; Ferritin_1.
DR	PS00204; Ferritin_2_1.
DR	PROSITE: PS50905; FERRITIN_LIKE_1.
DR	Hypothetical protein; Iron_Iron storage; Metal-binding.
SQ	SEQUENCE 183 AA; 20748 MW; E6AB306251D55106 CRC64;
Query	Match 84.7%; Score 728; DB 2; Length 183;
Best Local Similarity 80.6%; Pred. No. 1; 3e-52;	
Matches 141; Conservative 17; Mismatches 9; Indels 8; Gaps 1;	
KW	Hypothetical protein; Iron_Iron storage; Metal-binding.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	
DR	EMBL: K01930; AAA41154.1;
DR	HSSP: P29391; IIB3.
DR	InterPro: IPR001519; Ferritin.
DR	InterPro: IPR009078; Ferritin_RR_like.

DR InterPro; IPR00833; Ferritin_DpB.
 DR InterPro; IPR00940; Ferritin_Like.
 DR Pfam; PF00210; Ferritin_1.
 DR ProDom; PD000971; Ferritin_1.
 DR PROSITE; PS00540; FERRITIN_1; 1.
 DR PROSITE; PS00204; FERRITIN_2; 1.
 DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron; Iron storage; Metal-binding.
 FT INIT MET 0
 FT DOMAIN 6 155 Ferritin-like diiron.
 FT METAL 53 53 Iron (Potential).
 FT METAL 56 56 Iron (Potential).
 FT METAL 57 57 Iron (Potential).
 FT METAL 60 60 Iron (Potential).
 FT METAL 63 63 Iron (Potential).
 FT CONFLICT 97 97 E -> K (in Ref. 2).
 FT CONFLICT 120 121 RT -> OA (in Ref. 2).
 FT CONFLICT 125 125 L -> F (in Ref. 3).
 FT CONFLICT 154 154 V -> W (in Ref. 2).
 FT CONFLICT 155 155 Q -> A (in Ref. 3).
 SQ SEQUENCE 182 AA; MW: 3D3DEBC5B088655B CRC64;

Query Match 84.4%; Score 726; DB 1; Length 182;

Best Local Similarity 80.6%; Pred. No. 1.9e-52; Mismatches 9; Indels 8; Gaps 1;

Matches 141; Conservative 17; Query 1 YSTEVEAVNLVNLTYRASYTSLIGFYRDRDVALLEGVCHFFRELAEERKREGAERLJK 60
 Db 8 YSTEVEAVNLVNLTYRASYTSLIGFFFDRDVALLEGVCHFFRELAEERKREGAERLJK 67
 Query 61 MQNQRGGRALFQDQPSQDWGTPDAMKAIVLKSKLQALDLHALGSSKKADPHCD 120
 Db 68 IQNERGRGGRALFQDQPSQDWGKTEAMEALAKLNQALDLHALGSARTDPHCD 127
 Query 121 PLESHILDEEVKLKIKONGDHITNIQRLV-----KSAGGLGEVLFERILKHD 167
 Db 128 PLESHILDEEVKLKIKONGNHITNLARVOGPQPAQTVQAQSIGEYLFERILKHD 182

Search completed: August 22, 2005, 09:10:08
 Job time : 174 secs